

**BLAST Basic Local Alignment Search Tool**

- Your search is limited to records matching entrez query: Homo sapiens [ORGN].

Edit and Resubmit Save Search Strategies Formatting options Download

**Protein Sequence (430 letters)**

Results for: ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**  
Id|24806  
**Description**  
None  
**Molecule type**  
amino acid  
**Query Length**  
430

**Database Name**

nr

**Description**

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

**Program**

BLASTP 2.2.19+ Citation

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinhui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

**Reference - compositional score matrix adjustment**

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

Other reports: Search Summary [Taxonomy reports] [Distance tree of results]

**Search Parameters**

Program	blastp
Word size	3
Expect value	10
Hlist size	100
Gpositis	11,1
Metrics	BLOSUM62
Threshold	11
Composition-based stats	2
Filter string	F
Genetic Code	1
Window Size	40

**Database**

Posted date Feb 12, 2009 6:03 PM  
 Number of letters 2,713,143,868  
 Number of sequences 7,873,120  
 Entrez query Homo sapiens [ORGN]

**Karlin-Altschul statistics**

Params	Unaligned	Gapped
Lambda	0.326046	0.267
K	0.138029	0.041
H	0.443787	0.14

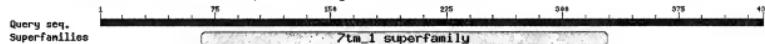
**Results Statistics**

Length adjustment 115  
 Effective length of query 315  
 Effective length of database 54918291  
 Effective search space 17299261665  
 Effective search space used 17299261665

**Graphic Summary**

Show Conserved Domains

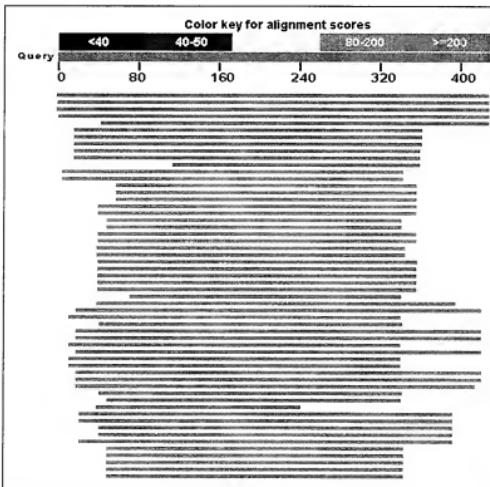
Putative conserved domains have been detected, click on the image below for detailed results.

**Distribution of 104 Blast Hits on the Query Sequence**

[?]

---

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



## Descriptions

Sequences producing significant alignments:	Score (Bits)	E Value	
ref NP_071429.1  neuropeptide FF receptor 1 [Homo sapiens] >...	881	0.0	MG
dbj RAC05950.1  seven transmembrane helix receptor [Homo sapi...	880	0.0	G
gb AAK94199.1  AF330055_1 neuropeptide NPVF receptor [Homo sap...	880	0.0	G
emb CA112599.1  neuropeptide FF receptor 1 [Homo sapiens]	877	0.0	G
gb EAM54387.1  neuropeptide FF receptor 1 [Homo sapiens]	789	0.0	G
ref NP_444264.1  neuropeptide FF receptor 2 isoform 2 [Homo s...	423	7e-118	MG
ref NP_001138228.1  neuropeptide FF receptor 2 isoform 3 [Homo...	422	1e-117	G
gb AAKS8513.1  AF236083_1 G-protein-coupled receptor 74 [Homo ...	422	2e-117	G
gb AAR22047.1  G-protein-coupled receptor [Homo sapiens]	420	4e-117	G
ref NP_004876.2  neuropeptide FF receptor 2 isoform 1 [Homo s...	420	4e-117	G
gb EAOX0547.1  neuropeptide FF receptor 2, isoform CRA_a [Hom...	286	1e-76	G
ref NP_001517.2  orexin receptor 2 [Homo sapiens] >sp 043614...	190	7e-48	G
gb AAC39602.1  orexin receptor-2; OX2R; G protein-coupled rec...	190	7e-48	G
gb AAC39601.1  orexin receptor-1; OX1R; G protein-coupled rec...	181	4e-45	G
ref NP_001516.2  orexin receptor 1 [Homo sapiens] >sp 043613...	179	2e-44	G
dbj RAS2120.1  unnamed protein product [Homo sapiens]	179	2e-44	G
ref NP_000901.1  neuropeptide Y receptor Y2 [Homo sapiens] >...	167	9e-41	UG
gb AAA3170.1  type 2 neuropeptide Y receptor	165	3e-40	G
ref NP_937822.2  G protein-coupled receptor 103 [Homo sapiens...]	165	3e-40	UG
dbj BAC98938.1  QRPF receptor [Homo sapiens]	164	4e-40	G
gb AAD00248.1  neuropeptide Y receptor type 2 [Homo sapiens]	164	5e-40	G
gb AAB07760.1  neuropeptide y/peptide YY receptor type 2	164	6e-40	G
gb AA559920.1  neuropeptide y receptor	160	8e-39	G
ref NP_000900.1  neuropeptide Y receptor Y1 [Homo sapiens] >...	160	1e-38	UG
gb AAP43705.1 AF236081_1 orphan G-protein coupled receptor GP...	156	1e-37	G
sp 09NYM4_2 GPR83_HUMAN RecName: Full=Probable G-protein coup...	156	1e-37	G
ref NP_057624.2  G protein-coupled receptor 83 [Homo sapiens...]	156	1e-37	UG
dbj BA96064.1  KIAA1540 protein [Homo sapiens]	156	1e-37	G
gb AAH67474.1  G protein-coupled receptor 83 [Homo sapiens]	152	2e-36	G
gb AAJ28134.1  GPR103 protein [Homo sapiens]	149	2e-35	G
ref NP_003848.1  galanin receptor 2 [Homo sapiens] >sp 043603...	148	3e-35	UG
gb AA05897.1  neurokinin-2 receptor	148	4e-35	G
gb AAH96367.1  Pancreatic polypeptide receptor 1 [Homo sapiens]	148	4e-35	G
ref NP_000721.1  cholecystokinin A receptor [Homo sapiens] >...	147	8e-35	UG
sp P21452.2 NGK2_HUMAN RecName: Full=Substance-K receptor; Sh...	146	1e-34	G
gb AAC31760.1  neurokinin A receptor [Homo sapiens] >gb AAK60...	145	3e-34	G
ref NP_005963.3  pancreatic polypeptide receptor 1 [Homo sapi...	145	3e-34	UG
ref NP_001048.2  tachykinin receptor 2 [Homo sapiens] >dbj BA...	145	3e-34	UG
gb AA07759.1  pancreatic polypeptide receptor >gb AAV68196.1...	145	3e-34	G
emb CAG6478.1  PYRY1 [Homo sapiens]	143	9e-34	G
gb EAM54325.1  tachykinin receptor 2, isoform CRA_b [Homo sap...	142	3e-33	G
gb AAH96842.1  Tachykinin receptor 2 [Homo sapiens]	140	9e-33	G
gb AAB20321.1  substance K receptor, SK receptor [human, Pep...	139	2e-32	G
prt AAI2648B.1 AF411117_1 G protein-coupled receptor [Homo sap...	137	6e-32	G
gb AAH24247.1  neuropeptide Y receptor Y1 variant [Homo sapi...	127	9e-29	G
gb AAZ22552.1  Tachykinin receptor 3 [Homo sapiens]	125	2e-28	G
gb AAB21706.1  neurokinin-3 receptor; NK-3 receptor [Homo sap...	125	2e-28	G
emb CNA46291.1  neuropeptidin K receptor [Homo sapiens]	125	3e-28	G
ref NP_001050.1  tachykinin receptor 3 [Homo sapiens] >sp P29...	125	3e-28	UG
gb AAH95527.1  TACR3 protein [Homo sapiens]	124	7e-28	G
sp Q13585.1 MTRRL_HUMAN RecName: Full=Melatonin-related recep...	123	1e-27	G
ref NP_004215.2  G protein-coupled receptor 50 [Homo sapiens]	123	1e-27	UG
gb AAI03697.1  GPR50 protein [Homo sapiens] >gb AAI05684.1  G...	122	2e-27	G
gb AAI05685.1  G protein-coupled receptor 50 [Homo sapiens] >...	122	2e-27	G
gb AAM99402.1  G protein-coupled receptor 50 [Homo sapiens]	122	2e-27	G
ref NP_0017128.1  bombesin-like receptor 3 [Homo sapiens] >sp ...	122	2e-27	UG
emb CGA6720.1  DRD1 [Homo sapiens]	122	2e-27	G
ref NP_001471.2  galanin receptor 1 [Homo sapiens]	122	2e-27	UG
sp P47211.1 GALR1_HUMAN RecName: Full=Galanin receptor type 1...	122	2e-27	G
emb CAA41734.1  D-1 dopamine receptor [Homo sapiens]	122	2e-27	G
gb AAKB3235.1 AF343725_1 G-protein-coupled receptor GPR54 [Ho...	122	2e-27	G

gb EAW61376.1	dopamine receptor D1, isoform CRA_a [Homo sapiens]	122	2e-27	G
ref NP_000785.1	dopamine receptor D1 [Homo sapiens] >sp P217...	122	2e-27	UG
gb AABE0356.1	galanin receptor >gb AAC95397.1  galanin recep...	122	3e-27	G
ref NP_115940.2	G protein-coupled receptor 54 [Homo sapiens]	122	3e-27	UG
prf  1614340X	dopamine receptor D1	120	6e-27	
dbj BAG36078.1	unnamed protein product [Homo sapiens]	117	5e-26	G
ref NP_001041.1	somatostatin receptor 2 [Homo sapiens] >sp P...	117	8e-26	UG
gb AA2A0828.1	somatostatin receptor	117	8e-26	G
ref NP_001044.1	somatostatin receptor 5 [Homo sapiens] >sp P...	117	9e-26	UG
ref NP_004239.1	G protein-coupled receptor 10 [Homo sapiens]	117	9e-26	UG
gb AAFA42810.1	[AF184174_2] somatostatin receptor 2B [Homo sapien...	116	1e-25	G
ref NP_658986.1	prokineticin receptor 2 [Homo sapiens] >sp Q...	116	1e-25	UG
gb EAX10422.1	prokineticin receptor 2 [Homo sapiens]	116	1e-25	G
dbj BAG36594.1	unnamed protein product [Homo sapiens]	116	2e-25	G
gb AAH5542.1	Neuromedin B receptor [Homo sapiens]	115	2e-25	G
gb ABQ52418.1	prokineticin receptor 2 [Homo sapiens]	115	2e-25	G
ref NP_002502.2	neuromedin B receptor [Homo sapiens] >sp P28...	115	3e-25	UG
gb AAJ59939.1	neuromedin B receptor >gb AA27330.1  neuromed...	115	3e-25	G
gb AAJ36623.1	somatostatin receptor >dbj AA04106.1  fourth ...	115	4e-25	G
gb AAKG1266.1	[AA06466.1] somatostatin receptor type 5 [Homo s...	115	4e-25	G
ref NP_005950.1	melatonin receptor 1B [Homo sapiens] >sp P49...	114	6e-25	UG
gb AAH09522.1	AAH09522 Unknown (protein for IMAGE:3354783) [H...	114	9e-25	G
ref NP_001043.2	somatostatin receptor 4 [Homo sapiens] >sp P...	113	1e-24	UG
gb AAW87342.1	DR kappa 1 splice variant KOR 1A [Homo sapiens]	113	1e-24	G
gb EAX10169.1	somatostatin receptor 4, isoform CRA_b [Homo s...	113	1e-24	G
emb CAH73066.1	prolactin releasing hormone receptor [Homo sa...	113	1e-24	G
dbj BAF82684.1	unnamed protein product [Homo sapiens]	113	1e-24	G
gb AA60565.1	somatostatin receptor	112	2e-24	G
dbj BAG60542.1	unnamed protein product [Homo sapiens]	110	6e-24	G
gb AAW21070.1	[AF498922_1] opioid receptor kappa [Homo sapiens]	110	6e-24	G
ref NP_000903.2	opioid receptor, kappa 1 [Homo sapiens] >sp ...	110	7e-24	UG
gb AAU32829.1	[AF441129_1] cholecystokinin-C receptor [Homo s...	110	8e-24	G
gb BAW6734.1	cholecystokinin B receptor, isoform CRA_a [Hom...	110	1e-23	G
gb EAX05261.1	G protein-coupled receptor 103, isoform CRA_a ...	110	1e-23	G
ref NP_795344.1	cholecystokinin B receptor [Homo sapiens] >s...	110	1e-23	UG
gb AAU30766.2	cholecystokinin B receptor [Homo sapiens]	109	1e-23	G
ref NP_001040.1	somatostatin receptor 1 [Homo sapiens] >sp P...	109	1e-23	UG
gb EAW68735.1	cholecystokinin B receptor, isoform CRA_b [Hom...	109	2e-23	G

#### Alignments Select All Get selected sequences Distance tree of results

```
>ref|NP_071429.1| UG neuropeptide FF receptor 1 [Homo sapiens]
sp|QBGZQ1.1|NPFF1_HUMAN G RecName: Full=Neuropeptide FF receptor 1; AltName: Full=G-protein
coupled receptor 147; AltName: Full=RFamide-related peptide
receptor OTTQ02
gb|AAH41397.1|AF266898_1 G neuropeptide FF receptor 1 [Homo sapiens]
dbj|BAB17677.1| G RFamide-related peptide receptor [Homo sapiens]
gb|AAJ131581.1| G Neuropeptide FF receptor 1 [Homo sapiens]
gb|ABY87527.1| G neuropeptide FF receptor 1 [Homo sapiens]
Length=430
```

Gene ID: 64106 NPFFR1 | neuropeptide FF receptor 1 [Homo sapiens]  
(10 or fewer PubMed links)

Score = 881 bits (2276), Expect = 0, Method: Compositional matrix adjust.  
Identities = 430/430 (100%), Positives = 430/430 (100%), Gaps = 0/430 (0%)

Query 1 MEGEPSPQPNPSNWPLQMQNTVTEATPATNVLTTSSYYQQTSPVAAAMPIVAYALIPLLCLMVG 60  
Sbjct 1 MEGEPSPQPNPSNWPLQMQNTVTEATPATNVLTTSSYYQQTSPVAAAMPIVAYALIPLLCLMVG 60

Query 61 NTLLACPIVLLKNNHHHTVTTNNFLMLLJLVSDLJLWV1FCMPDTTLVWNLITLGMPDNATCKNSG 120  
Sbjct 61 NTLLACPIVLLKNNHHHTVTTNNFLMLLJLVSDLJLWV1FCMPDTTLVWNLITLGMPDNATCKNSG 120

Query 121 LVQOMGSVASVFTLVAIAVERPVC1VHPFREKLTLKRALVTIAVIALALLJMCPSAVTL, 180  
Sbjct 121 LVQOMGSVASVFTLVAIAVERPVC1VHPFREKLTLKRALVTIAVIALALLJMCPSAVTL, 180

Query 181 TVTREEHHPFWDAARNNSYPLYSCEAMPEKGMRGRVVTTTVLFSHYYLAPLALIVMMYARIA 240  
Sbjct 181 TVTREEHHPFWDAARNNSYPLYSCEAMPEKGMRGRVVTTTVLFSHYYLAPLALIVMMYARIA 240

Query 241 RKLQCAPOGPGEEEAADPRASRRARVYIIMLMVWVNLFPTLSWLPLMWALLLLLIDYQQLSA 300  
Sbjct 241 RKLQCAPOGPGEEEAADPRASRRARVYIIMLMVWVNLFPTLSWLPLMWALLLLLIDYQQLSA 300

Query 301 PQLHLVTVVAPPPAHMLAFFFNSSANIYIGYNENPRRGPOAAPFARLCPRPGSGSHKEY 360  
 Sbjct 301 PCMLHVTVVAPPPAHMLAFFFNSSANIYIGYNENPRRGPOAAPFARLCPRPGSGSHKEY 360

Query 361 SERPOGILLHRVFPVVVRPSDGLPSESPGSQAPRPGRLPLRNGRVAHHGLPREPGCASH 420  
 Sbjct 361 SERPOGILLHRVFPVVVRPSDGLPSESPGSQAPRPGRLPLRNGRVAHHGLPREPGCASH 420

Query 421 LPITIPAMDI 430  
 Sbjct 421 LPITIPAMDI 430

>dbj|BAC05950.1| C seven transmembrane helix receptor [Homo sapiens]  
 Length=441

Gene ID: 64106 NPFFR1 | neuropeptide FF receptor 1 [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 880 bits (2274), Expect = 0.0, Method: Compositional matrix adjust.  
 Identities = 429/429 (100%), Positives = 429/429 (100%), Gaps = 0/429 (0%)

Query 2 EGEPSPQPNSSWPLSQNQTNTTEATPATNLTFSSYYQHTSPVAAAMPIVAYALILFLCMVG 61  
 EGEPSPQPNSSWPLSQNQTNTTEATPATNLTFSSYYQHTSPVAAAMPIVAYALILFLCMVG 72

Query 62 TLVCFIVLXNRBHMTTINPMFLNLAWSLDLW1G1FCMPPTTLVONLITCPFDNACTKMSG 121  
 TLVCFIVLXNRBHMTTINPMFLNLAWSLDLW1G1FCMPPTTLVONLITCPFDNACTKMSG 132

Sbjct 73 TLVCFIVLXNRBHMTTINPMFLNLAWSLDLW1G1FCMPPTTLVONLITCPFDNACTKMSG 132

Query 122 VQGMGSVASVPTLVAVIAVERPRCIVHPREKUJTRKALVTTIATIVIMALALLIMCPSPAVLT 181  
 VQGMGSVASVPTLVAVIAVERPRCIVHPREKUJTRKALVTTIATIVIMALALLIMCPSPAVLT 181

Sbjct 133 VQGMGSVASVPTLVAVIAVERPRCIVHPREKUJTRKALVTTIATIVIMALALLIMCPSPAVLT 192

Query 182 VTREEHHPMVDARNSPYLSMCWEMPERGMRVTTTFLPSH1YLAPLAIVVMYARIA 241  
 VTREEHHPMVDARNSPYLSMCWEMPERGMRVTTTFLPSH1YLAPLAIVVMYARIA 252

Sbjct 193 VTREEHHPMVDARNSPYLSMCWEMPERGMRVTTTFLPSH1YLAPLAIVVMYARIA 252

Query 242 KLCQAPGPAAGGEAADPDRASRRARVHML/WALPFTLSWLPIWALLLLIDYQQLSAP 301  
 KLCQAPGPAAGGEAADPDRASRRARVHML/WALPFTLSWLPIWALLLLIDYQQLSAP 312

Sbjct 253 KLCQAPGPAAGGEAADPDRASRRARVHML/WALPFTLSWLPIWALLLLIDYQQLSAP 312

Query 303 QLHLVTVVAPPPAHMLAFFFNSSANIYIGYNENPRRGPOAAPFARLCPRPGSGSHKEYS 361  
 Sbjct 313 QLHLVTVVAPPPAHMLAFFFNSSANIYIGYNENPRRGPOAAPFARLCPRPGSGSHKEYS 372

Query 362 ERPGGLLHRRVFPVVVRPSDGLPSESPGSQAPRPGRLPLRNGRVAHHGLPREPGCASH 421  
 Sbjct 373 ERPGGLLHRRVFPVVVRPSDGLPSESPGSQAPRPGRLPLRNGRVAHHGLPREPGCASH 432

Query 422 PLTIPAMDI 430  
 Sbjct 433 PLTIPAMDI 441

>gb|AKM94199.1|AF330055.1 C neuropeptide NPVF receptor [Homo sapiens]  
 Length=430

Gene ID: 64106 NPFFR1 | neuropeptide FF receptor 1 [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 880 bits (2273), Expect = 0.0, Method: Compositional matrix adjust.  
 Identities = 429/430 (99%), Positives = 429/430 (99%), Gaps = 0/430 (0%)

Query 1 MEGEPSPQPNSSWPLSQNQTNTTEATPATNLTFSSYYQHTSPVAAAMPIVAYALILFLCMVG 60  
 MEGEPSPQPNSSWPLSQNQTNTTEATPATNLTFSSYYQHTSPVAAAMPIVAYALILFLCMVG 60

Sbjct 1 MEGEPSPQPNSSWPLSQNQTNTTEATPATNLTFSSYYQHTSPVAAAMPIVAYALILFLCMVG 60

Query 61 NTLCFIVLXNRBHMTTINPMFLNLAWSLDLW1G1FCMPPTTLVONLITCPFDNACTKMSG 120  
 NTLCFIVLXNRBHMTTINPMFLNLAWSLDLW1G1FCMPPTTLVONLITCPFDNACTKMSG 120

Sbjct 61 NTLCFIVLXNRBHMTTINPMFLNLAWSLDLW1G1FCMPPTTLVONLITCPFDNACTKMSG 120

Query 121 LVQGMGSVASVPTLVAVIAVERPRCIVHPREKUJTRKALVTTIATIVIMALALLIMCPSPAVTL 180  
 Sbjct 121 LVQGMGSVASVPTLVAVIAVERPRCIVHPREKUJTRKALVTTIATIVIMALALLIMCPSPAVTL 180

Query 181 TTPEHHPMVDARNSPYLSMCWEMPERGMRVTTTFLPSH1YLAPLAIVVMYARIA 240  
 TTPEHHPMVDARNSPYLSMCWEMPERGMRVTTTFLPSH1YLAPLAIVVMYARIA 240

Sbjct 181 TTPEHHPMVDARNSPYLSMCWEMPERGMRVTTTFLPSH1YLAPLAIVVMYARIA 240

Query 241 RKLCOAPGPAAGGEAADPDRASRRARVHML/WALPFTLSWLPIWALLLLIDYQQLSA 300  
 RKLCOAPGPAAGGEAADPDRASRRARVHML/WALPFTLSWLPIWALLLLIDYQQLSA 300

Sbjct 241 RKLCOAPGPAAGGEAADPDRASRRARVHML/WALPFTLSWLPIWALLLLIDYQQLSA 300

Query 301 PQHLVTVVAPPPAHMLAFFFNSSANIYIGYNENPRRGPOAAPFARLCPRPGSGSHKEY 360  
 Sbjct 301 PQHLVTVVAPPPAHMLAFFFNSSANIYIGYNENPRRGPOAAPFARLCPRPGSGSHKEY 360

Query 361 SERPOGILLHRVFPVVVRPSDGLPSESPGSQAPRPGRLPLRNGRVAHHGLPREPGCASH 420  
 SERPOGILLHRVFPVVVRPSDGLPSESPGSQAPRPGRLPLRNGRVAHHGLPREPGCASH 420

Sbjct 361 SERPOGILLHRVFPVVVRPSDGLPSESPGSQAPRPGRLPLRNGRVAHHGLPREPGCASH 420

Query 421 LPITIPAMDI 430  
 Sbjct 421 LPITIPAMDI 430

>emb|CA112599.1| C neuropeptide FF receptor 1 [Homo sapiens]  
 Length=428

Gene ID: 64106 NPFFR1 | neuropeptide FF receptor 1 [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 877 bits (2265), Expect = 0.0, Method: Compositional matrix adjust.  
 Identities = 428/428 (100%), Positives = 428/428 (100%), Gaps = 0/428 (0%)

Query 3 GEPSQPPNSWPLSQNQTNTTEATPATNLTFSSYYQHTSPVAAAMPIVAYALILFLCMVGNT 62  
 GEPSQPPNSWPLSQNQTNTTEATPATNLTFSSYYQHTSPVAAAMPIVAYALILFLCMVGNT

Sbjct	1	GEPSQPNNPSWPLSQNGNTTEATPATNLTFSSYYQPTSPVAAIFIYVALIFLFLCHVGNT	60
Query	63	LVCVFLVNRKMRHETVTNNFTFLA8WSVLDL1GIFCMPPTLVNDL1TGWPFDNATCNGSLV	122
Sbjct	1	LVCVFLVNRKMRHETVTNNFTFLA8WSVLDL1GIFCMPPTLVNDL1TGWPFDNATCNGSLV	120
Sbjct	61	LVCVFLVNRKMRHETVTNNFTFLA8WSVLDL1GIFCMPPTLVNDL1TGWPFDNATCNGSLV	120
Query	123	QGSNSVASPFTVLLA1VA1VERPRC1V8PKEKRLT1KLAVLTIA1NAL1LINCSPVATLTV	170
Sbjct	121	QGSNSVASPFTVLLA1VA1VERPRC1V8PKEKRLT1KLAVLTIA1NAL1LINCSPVATLTV	180
Query	183	TREHEHMMRNPNSRSYPLSYCEMABPGRGGRRVTTTFLVSHIYLAPLAL1VWYHARIAK	242
Sbjct	181	TREHEHMMRNPNSRSYPLSYCEMABPGRGGRRVTTTFLVSHIYLAPLAL1VWYHARIAK	240
Query	243	LQCGGPRGGEEAADPGRASRERVAVHMLVMVALFTPSLWMLALLLIDYQGQSAQ	300
Sbjct	241	LQCGGPRGGEEAADPGRASRERVAVHMLVMVALFTPSLWMLALLLIDYQGQSAQ	300
Query	303	LHVVTVFAAFAFPFHAAFLFNSNSANP1IYGFYFRRPBPQAFARFL1PPPSGSHAYES	362
Sbjct	301	LHVVTVFAAFAFPFHAAFLFNSNSANP1IYGFYFRRPBPQAFARFL1PPPSGSHAYES	360
Query	363	RPGQLLRRHVVYVVFSPBGLPSESSPQAFARFL1PLRNGRVRVHHLGPREQPCSHLP	422
Sbjct	361	RPGQLLRRHVVYVVFSPBGLPSESSPQAFARFL1PLRNGRVRVHHLGPREQPCSHLP	420
Query	423	LTP1PANDI 430	
Sbjct	421	LTP1PANDI 428	

>gb|EAW54387.1| G neuropeptide FF receptor 1 [Homo sapiens]  
Length=386

Score = 789 bits (2037), Expect = 0.0, Method: Compositional matrix adjust Identities = 366/386 (10%), Positives = 386/386 (100%), Gaps = 0/386 (0%)	
Query 45	NFIVAYALIPLFLCNCVNTLVLFCVILNREHNRHHTVNFLINAVLSDLSVGLVCPMTLVND
Sbjct 1	NFIVAYALIPLFLCNCVNTLVLFCVILNREHNRHHTVNFLINAVLSDLSVGLVCPMTLVND
Query 105	LITGWPFDNATCAGSLVQGNSVASVTPFLTLVAIAVERFCIVIHPFPREKLRLKRALVTIV
Sbjct 61	LITGWPFDNATCAGSLVQGNSVASVTPFLTLVAIAVERFCIVIHPFPREKLRLKRALVTIV
Query 165	IWALALLIMCPASVLTITVTEHHWPMDDARNSRPLSYLSWCHEAMPEPKGRVRYYTFLVSHI
Sbjct 121	IWALALLIMCPASVLTITVTEHHWPMDDARNSRPLSYLSWCHEAMPEPKGRVRYYTFLVSHI
Query 225	YIPLALPLALIVMAYERIAIRKLCQPGAPGGEAEADPRASRRARVHJHMLWVAPFTLWSL
Sbjct 181	YIPLALPLALIVMAYERIAIRKLCQPGAPGGEAEADPRASRRARVHJHMLWVAPFTLWSL
Query 285	PLMLMLLLIDYQPSOLHIIYUITYPAPFHMLWFNSPAMG1IYGGNFNRPRCOPAFL
Sbjct 241	PLMLMLLLIDYQPSOLHIIYUITYPAPFHMLWFNSPAMG1IYGGNFNRPRCOPAFL
Query 345	RARLCPGPPSGHSIKAYSERPPOGLLHRVVFVVRPDRSGLPGRSEGSQSSGA_PPCPRLRNG
Sbjct 301	RARLCPGPPSGHSIKAYSERPPOGLLHRVVFVVRPDRSGLPGRSEGSQSSGA_PPCPRLRNG
Query 405	RVNNHGLPREDQSCSLLH17LP1PMD1 430
Sbjct 361	RVNNHGLPREDQSCSLLH17LP1PMD1 386

```

>refNP_444264.1 | UG neuropeptide FF receptor 2 isoform 2 [Homo sapiens]
|gb|AAF87078.1 | G G-protein coupled receptor HLWARR7 [Homo sapiens]
|gb|AAG4196.1 | G neuropeptide FF receptor 2 [Homo sapiens]
|gb|AKX94197.1 | PFJ330053.1 | G neuropeptide NPFF receptor [Homo sapiens]
|gb|BAE05648.1 | G neuropeptide FF receptor 2, isoform CRA_b [Homo sapiens]
|gb|AAU1314.2 | G Neuropeptide FF receptor 2 [Homo sapiens]
|gb|AAU10637.1 | G Neuropeptide FF receptor 2 [Homo sapiens]
|dbsj|BAP83626.1 | G unnamed protein product [Homo sapiens]
Length=429

```

Query 316 WLAFFNNSSANPIIYGYNENFRRGFQAAFRARLCPRPGSHKEAYER 363  
 Sbjct 320 WLAFFNNSVNPVIIYGYNENFRRGFQEAFOQLCQKRKAP-MEAYALK 366

>gb|NP\_001138228.1| **G** neuropeptide FF receptor 2 isoform 3 [Homo sapiens]  
 gbi|EAX05650.1| **G** neuropeptide FF receptor 2, isoform CRA\_d [Homo sapiens]  
 Length=423  
 Gene ID: 10886 NPFFR2 | neuropeptide FF receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 422 bits (1085), Expect = 1e-117, Method: Compositional matrix adjust.  
 Identities = 197/348 (56%), Positives = 265/348 (76%), Gaps = 3/348 (0%)  
 Query 18 NGNTTATPATNLTFSSTYYQTSPVAAMPIVAYALIPLLCNGNTLVCFIVLNRRHMTV 77  
 N T- + \*Y H VAA+FI+\*Y LIF LCM+GNT+VCPIV++N+HMTV  
 Sbjct 23 NDTHKHLYSDINITYVNYYLHQPOVQAIFIISYPLIFLICMNGNTVVCFIVMRNNHMTV 82  
 Query 78 TMPIFLNLASDLWLGIPCMPTTLVDNLITLTGMPFDNATCMMGGLVQGMSVASVFTLVAI 137  
 TM+FLNLAS+SDLWLGIPCMPTTL-DN+I GMPP N CK+SGLVGQ-SV+ASVFTLVAI  
 Sbjct 83 TMPIFLNLASDLWLGIPCMPTTLVDNLITLTGMPFDNATCMMGGLVQGMSVASVFTLVAI 142  
 Query 138 AVERFCRIVHPFPREKLTLRKALVLTAVIAVIALALLIMCPASAVTIVTREBHHPM-VDARNN 196  
 AV+RF-CV+PF+ KLT+A V I + IM LA+ IM PSAV L V E+++ + ++++N+  
 Sbjct 143 AVDRFCQCVVPPFKPLGTAKTAVIIMVIIWLAITIMPSAVMLHVQEKKYVRRLNSQN 202  
 Query 197 SYPLSYCWEAWPEKGMRVTVFPHSIYLAPALIIVWYARIARLKLQCAPGPAGGEAA 256  
 + PY C E WE + MR++YTTFVLP+IYLAPL+LIV-MY RI L +A P G +  
 Sbjct 203 TSPVYHCREDWPNEMRKYIYTFLPANFYIYLAPLSLIVIMYGRIGISLFRAPVHTGRKQ 262  
 Query 257 ADPR-ASERRARVVRHMLWVLAFFPFLSPLWPLALLLDYDQPAQHLYLVTVYAPPFAN 315  
 SR+ + ++ ML+WF A LSRPLPW L++L DY LS +L ++ + Y+PFAN  
 Sbjct 263 EQWHVVSRRKQKIIKDLJLWPLVLLWPLWPLWPLMTMLSDYADLSPLNQLIIINIIYYPFAH 322  
 Query 316 WLAFFNNSANPIIYGYNENFRRGFQAAFRARLCPRPGSHKEAYER 363  
 Sbjct 323 WLAFFNNSVNPVIIYGYNENFRRGFQEAFOQLCQKRKAP-MEAYALK 369

>gb|AAK58513.1| **G** G-protein-coupled receptor 74 [Homo sapiens]  
 Length=408  
 Gene ID: 10886 NPFFR2 | neuropeptide FF receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 422 bits (1084), Expect = 2e-117, Method: Compositional matrix adjust.  
 Identities = 197/348 (56%), Positives = 265/348 (76%), Gaps = 3/348 (0%)  
 Query 18 NGNTTATPATNLTFSSTYYQTSPVAAMPIVAYALIPLLCNGNTLVCFIVLNRRHMTV 77  
 N T- + \*Y H VAA+FI+\*Y LIF LCM+GNT+VCPIV++N+HMTV  
 Sbjct 23 NDTHGHLYSDINITYVNYYLHQPOVQAIFIISYPLIFLICMNGNTVVCFIVMRNNHMTV 82  
 Query 78 TMPIFLNLASDLWLGIPCMPTTLVDNLITLTGMPFDNATCMMGGLVQGMSVASVFTLVAI 137  
 TM+FLNLAS+SDLWLGIPCMPTTL-DN+I GMPP N CK+SGLVGQ-SV+ASVFTLVAI  
 Sbjct 83 TMPIFLNLASDLWLGIPCMPTTLVDNLITLTGMPFDNATCMMGGLVQGMSVASVFTLVAI 142  
 Query 138 AVERFCRIVHPFPREKLTLRKALVLTAVIAVIALALLIMCPASAVTIVTREBHHPM-VDARNN 196  
 AV+RF-CV+PF+ KLT+A V I + IM LA+ IM PSAV L V E+++ + ++++N+  
 Sbjct 143 AVDRFCQCVVPPFKPLGTAKTAVIIMVIIWLAITIMPSAVMLHVQEKKYVRRLNSQN 202  
 Query 197 SYPLSYCWEAWPEKGMRVTVFPHSIYLAPALIIVWYARIARLKLQCAPGPAGGEAA 256  
 + PY C E WE + MR++YTTFVLP+IYLAPL+LIV-MY RI L +A P G +  
 Sbjct 203 TSPVYHCREDWPNEMRKYIYTFLPANFYIYLAPLSLIVIMYGRIGISLFRAPVHTGRKQ 262  
 Query 257 ADPR-ASERRARVVRHMLWVLAFFPFLSPLWPLALLLDYDQPAQHLYLVTVYAPPFAN 315  
 SR+ + ++ ML+WF A LSRPLPW L++L DY LS +L ++ + Y+PFAN  
 Sbjct 263 EQWHVVSRRKQKIIKDLJLWPLVLLWPLWPLMTMLSDYADLSPLNQLIIINIIYYPFAH 322  
 Query 316 WLAFFNNSANPIIYGYNENFRRGFQAAFRARLCPRPGSHKEAYER 363  
 Sbjct 323 WLAFFNNSVNPVIIYGYNENFRRGFQEAFOQLCQKRKAP-MEAYALK 369

>gb|AA23047.1| **G** G-protein-coupled receptor [Homo sapiens]  
 Length=522  
 Gene ID: 10886 NPFFR2 | neuropeptide FF receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 420 bits (1080), Expect = 4e-117, Method: Compositional matrix adjust.  
 Identities = 197/346 (56%), Positives = 264/346 (76%), Gaps = 3/346 (0%)  
 Query 18 NGNTTATPATNLTFSSTYYQTSPVAAMPIVAYALIPLLCNGNTLVCFIVLNRRHMTV 77  
 N T- + \*Y H VAA+FI+\*Y LIF LCM+GNT+VCPIV++N+HMTV  
 Sbjct 122 NDTHGHLYSDINITYVNYYLHQPOVQAIFIISYPLIFLICMNGNTVVCFIVMRNNHMTV 181  
 Query 78 TMPIFLNLASDLWLGIPCMPTTLVDNLITLTGMPFDNATCMMGGLVQGMSVASVFTLVAI 137  
 TM+FLNLAS+SDLWLGIPCMPTTL-DN+I GMPP N CK+SGLVGQ-SV+ASVFTLVAI  
 Sbjct 182 TMPIFLNLASDLWLGIPCMPTTLVDNLITLTGMPFDNATCMMGGLVQGMSVASVFTLVAI 241  
 Query 138 AVERFCRIVHPFPREKLTLRKALVLTAVIAVIALALLIMCPASAVTIVTREBHHPM-VDARNN 196  
 AV+RF-CV+PF+ KLT+A V I + IM LA+ IM PSAV L V E+++ + ++++N+  
 Sbjct 242 AVDRFCQCVVPPFKPLGTAKTAVIIMVIIWLAITIMPSAVMLHVQEKKYVRRLNSQN 301  
 Query 197 SYPLSYCWEAWPEKGMRVTVFPHSIYLAPALIIVWYARIARLKLQCAPGPAGGEAA 256  
 + PY C E WE + MR++YTTFVLP+IYLAPL+LIV-MY RI L +A P G +  
 Sbjct 302 TSPVYHCREDWPNEMRKYIYTFLPANFYIYLAPLSLIVIMYGRIGISLFRAPVHTGRKQ 361  
 Query 257 ADPR-ASERRARVVRHMLWVLAFFPFLSPLWPLALLLDYDQPAQHLYLVTVYAPPFAN 315  
 SR+ + ++ ML+WF A LSRPLPW L++L DY LS +L ++ + Y+PFAN  
 Sbjct 362 EQWHVVSRRKQKIIKDLJLWPLVLLWPLWPLMTMLSDYADLSPLNQLIIINIIYYPFAH 421  
 Query 316 WLAFFNNSANPIIYGYNENFRRGFQAAFRARLCPRPGSHKEAYER 361  
 Sbjct 422 WLAFFNNSVNPVIIYGYNENFRRGFQEAFOQLCQKRKAP-MEAYT 466



Query 270 HMLWVVALFPTLSQLPLWALLLLIDYQQLSAPOLHLTVYA-FPPAHMLAFLFNSSANPII 328  
 ML++V L F + +L+P L + L + A TVYA F F+HML + NS+ANPII 328  
 Sbjct 304 RMLMVVLLWFAICYLPISILNVLKRVFGMFAHTEDETRVYAMPTFSHMLVYVANSAAANPII 363  
 Query 329 YGYVNENFRGQOAF 344  
 Sbjct 364 YNPLSGKPRKEEKFKA 379

>gb|AAC39602.1| **G** orexin receptor-2; OX2R; G protein-coupled receptor [Homo sapiens]  
 gb|ANG28021.1| **G** hypocretin receptor-2 [Homo sapiens]  
 gb|AAL47215.1| **G** hypocretin receptor-2; orexin receptor 2 [Homo sapiens]  
 dbj|BAG36939.1| **G** unnamed protein product [Homo sapiens]  
 Length=444

Gene ID: 3062 HCSTR2 | hypocretin (orexin) receptor 2 [Homo sapiens]

Score = 190 bits (483), Expect = 7e-48, Method: Compositional matrix adjust.  
 Identities = 128/376 (34%), Positives = 189/376 (50%), Gaps = 41/376 (10%)

Query 6 SQPFNSWPLSQNGNTTAA-----TPATPLHTFSEY---YQHTSPVAANPFIYAVAYLFL 56  
 Sbjct 8 DSPFCRNNSASSELNETPQFLNPJTDYDDEFLPFLYRLREYLHKEYEWVILAGIYIIVFV 67  
 Query 57 CNGNTLAVCFVLUKNRHMHTVTNMFTILAVSDLLWGCPTC/PPTLVLVNDLITGMPPDNATC 116  
 +GR LVC V KN HEH TTVN F+NL++D+LV I+C+P TL+ + +W P+ + C  
 Sbjct 68 ALIGNVLCVVAWVKHNHHMETVNTYVFLVNLISLADLVLTICLCPATLWDITSTTQGQSLC 127  
 Query 117 KMSGLQKQGNSVSAASGVPTLAVLAVERPFCIVHPPTREKULTRAKALVTFINIVIALLIMCPS 176  
 X+ +O +GVA SV TL +A+R + I HE K T+A +I +W + + +IM P  
 Sbjct 128 KVIPLQLOTVSVSVSVLTLSCILADWVYAIChPLMPKSTAKRARSIIIVIWSICIMIPQ 187  
 Query 177 ATVLTVTREHHHFVWVARNRSYPLVSCHENPEKMRVTVTFLPSHYIPLAPALIIVVWY 236  
 A+ + E N++ C E M + +Y F YAPL L+V+ Y  
 Sbjct 188 AIVM---ECSTVPFLANKNTLPTVCDERMGGEEVPMYHICFFLVTVMAPLCLMVLAY 243  
 Query 237 +ARIKXL\_C QPGP+ -----PG-----GEAADPRASTRRARV 269  
 Sbjct 244 LOIFRKWLNCRQ1PGTSSVVQWRKWPQLQPSQPROQQPTSKSRMGAVAEAEIKQRARRKTA 303  
 Query 270 HMLWVVALFPTLSQLPLWALLLLIDYQQLSAPOLHLTVYA-FPPAHMLAFLFNSSANPII 328  
 ML++V L F + +L+P L + L + A TVYA F F+HML + NS+ANPII 328  
 Sbjct 304 RMLMVVLLWFAICYLPISILNVLKRVFGMFAHTEDETRVYAMPTFSHMLVYVANSAAANPII 363  
 Query 329 YGYVNENFRGQOAF 344  
 Sbjct 364 YNPLSGKPRKEEKFKA 379

>gb|AAC39601.1| **G** orexin receptor-1; OXIR; G protein-coupled receptor [Homo sapiens]  
 Length=425

Gene ID: 3061 HCSTR1 | hypocretin (orexin) receptor 1 [Homo sapiens]

Score = 181 bits (459), Expect = 4e-45, Method: Compositional matrix adjust.  
 Identities = 122/341 (35%), Positives = 171/341 (50%), Gaps = 46/341 (13%)

Query 60 GNTLVCFTVLKRNRMHTVTNMFTILAVSDLLWGCPTC/PPTLVLVNDLITGMPPDNATCNS 119  
 GNTLVC V +BN TVN F+NL++D+LV C+P +L+ + + W F +A CK+  
 Sbjct 63 GNTLVCCLAVRNRRHMHTVTYVFLVNLISLADLVLTICLCPASLVDITSTTQGQSLC 122  
 Query 120 GLVGXGSVSAFPTLAVLAVERPFCIVHPPTREKULTRAKALVTFINIVIALLIMCPSVT 179  
 Q+G+S+V TL +A+R + I HP K T R+A +I IWA+L IN P A  
 Sbjct 123 PYLQAQSVAWSVAVLTLPSHNAWICHPKSTAKRARSIIIVIWSICIMIPQ 182  
 Query 180 LT+VREHHHFVWVARNRSYPLVSCHENPEKMRVTVTFLPSHYIPLAPALIIVVWYRI 239  
 + E + + NR+ C E M + +Y + F YAPL L+ + Y + I  
 Sbjct 183 M---ECSSVLPFLANKNTLPTVCDERMADOLYPKTYHSCPFIVTVLAPLQIWMAMAYPQI 238  
 Query 240 ARKLX\_C-QAPG-----PANGGE-AADPRASTRRARV 270  
 Sbjct 239 FAKRQK\_C QAPG-----PANGGE-AADPRASTRRARV  
 Sbjct 240 PGTTSALVANWKPSDQQLDGLBQCLSEQEPYQROQNFUVEKQGRARRKTK 298  
 Query 271 MLWVVALFPTLSQLPLWALLLLIDYQQLSAPOLHLTVYA-FPPAHMLAFLFNSSANPII 329  
 ML++V L F + +L+P L + L + A TVYA F F+HML + NS+ANPII 329  
 Sbjct 299 MDMVWVLLWFAICYLPISILNVLKRVFGMFAHTEDETRVYAMPTFSHMLVYVANSAAANPII 358  
 Query 330 GYFVNENFRGQOAFPARL-----CPRPGSHKE 358  
 Sbjct 359 NFPLSGKPRKEEKFKA 399

>ref|NP\_001516.2| **G** orexin receptor 1 [Homo sapiens]  
 sp|043613.2|OXLR\_HUMAN **G** RecName: Full=Orexin receptor type 1; AltName: Full=Oxlr; AltName: Full=Hypocretin receptor type 1  
 gb|ANG28020.1| **G** hypocretin receptor-1 [Homo sapiens]  
 gb|AAL47214.1| **G** hypocretin receptor 1; orexin receptor 1 [Homo sapiens]  
 gb|AAL50221.1| **G** hypocretin receptor 1 [Homo sapiens]  
 gb|AAN74796.1| **G** Hypocretin (orexin) receptor 1 [Homo sapiens]  
 gb|BAX07602.1| **G** hypocretin (orexin) receptor 1, isoform CRA\_c [Homo sapiens]  
 Length=425

Gene ID: 3061 HCSTR1 | hypocretin (orexin) receptor 1 [Homo sapiens]

Score = 179 bits (453), Expect = 2e-44, Method: Compositional matrix adjust.  
 Identities = 122/341 (35%), Positives = 171/341 (50%), Gaps = 46/341 (13%)

Query 60 GNTLVCFTVLKRNRMHTVTNMFTILAVSDLLWGCPTC/PPTLVLVNDLITGMPPDNATCNS 119

GNTLVC V +N HM TVTN FI+NL++D-LV C+P L+ + + W F +A CK+  
 Sbjct 63 GNTLVC LAVNRNHMRTTVTNPIVNLSLADVLTAICLPA SLVDITESMLFGHALCKVI 122  
 Query 120 GLVQMSVSASVPTLA VAI AVERP CIVHPPRERLTLKALVTTAVIAVALI ALI MCPSAVT 179  
 Sbjct 123 Q+SVS +V TL IA+RA I HD K+R + - IMA+I LM P A 182  
 Sbjct 183 PYLQA SVS VAVL TLTSPLNRLWYAI CHPLLFSTARRARGSLSLGIWASLAIMVPOAAV 182  
 Query 180 LTVTREHHNFWDARNSSYLSCWAMPKGMHRVTTFLSHIYLAPLALI VVMVARI 239  
 Sbjct 183 M--- ECSSVLP E LANTRLPSV CDE RADDLYPKYIHS CFCFIVTVYLA PLGQIYAMAYFOI 238  
 Query 240 ARHL-C-QAPGPAPG----- GREAAD----- PRAS----- RRARAVH 270  
 Sbjct 239 RKL Q PG + + D PRA R R +  
 PRKLMGRQIOPGTTSALVRNMKPRSDQQLGDLSQQLSGEPCPQPRARAFALAEVKQMARRKTAK 298  
 Query 271 MLVWVALPFTLSLWLMWALLL LIDYQGOLSLPAOLHIVTVVA -PPFAHWLAFPN SANPIIY 329  
 Sbjct 299 MLVWVALPFTLSLWLMWALLL LIDYQGOLSLPAOLHIVTVVA -PPFAHWLAFPN SANPIIY 358  
 Query 330 GYFNENFRRGPFQAPARL----- CPRPGSSHE 358  
 Sbjct 359 NFLSGKFREQKAFASSCLPGLCPGSLXAPSPRSASHKS 399

>obj|BAF83210.1| **C** unnamed protein product [Homo sapiens]

Length=425

Gene ID: 3061 HCRTR1 | hypocretin (orexin) receptor 1 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 179 bits (453), Expect = 2e-44, Method: Compositional matrix adjust.  
 Identities = 122/341 (35%), Positives = 171/341 (50%), Gaps = 46/341 (13%)  
 Query 60 GNTLVC TFLNENHMRTTVTNPIVNLSLADVLJGICFMPTLVNDLITQCMWFDUNATCWS 119  
 Sbjct 63 GNTLVC LAVNRNHMRTTVTNPIVNLSLADVLTAICLPA SLVDITESMLFGHALCKVI 122  
 Query 120 GLVQMSVSASVPTLA VAI AVERP CIVHPPRERLTLKALVTTAVIAVALI ALI MCPSAVT 179  
 Sbjct 123 Q+SVS +V TL IA+RA I HD K+R + - IMA+I LM P A 182  
 Sbjct 183 PYLQA SVS VAVL TLTSPLNRLWYAI CHPLLFSTARRARGSLSLGIWASLAIMVPOAAV 182  
 Query 180 LTVTREHHNFWDARNSSYLSCWAMPKGMHRVTTFLSHIYLAPLALI VVMVARI 239  
 Sbjct 183 M--- ECSSVLP E LANTRLPSV CDE RADDLYPKYIHS CFCFIVTVYLA PLGQIYAMAYFOI 238  
 Query 240 ARHL-C-QAPGPAPG----- GREAAD----- PRAS----- RRARAVH 270  
 Sbjct 239 PRKLMGRQIOPGTTSALVRNMKPRSDQQLGDLSQQLSGEPCPQPRARAFALAEVKQMARRKTAK 298  
 Query 271 MLVWVALPFTLSLWLMWALLL LIDYQGOLSLPAOLHIVTVVA -PPFAHWLAFPN SANPIIY 329  
 Sbjct 299 MLVWVALPFTLSLWLMWALLL LIDYQGOLSLPAOLHIVTVVA -PPFAHWLAFPN SANPIIY 358  
 Query 330 GYFNENFRRGPFQAPARL----- CPRPGSSHE 358  
 Sbjct 359 NFLSGKFREQKAFASSCLPGLCPGSLXAPSPRSASHKS 399

>ref|NP\_000901.1| **C** neuropeptide Y receptor Y2 [Homo sapiens]

sp|P49146.1|NPY2\_R\_HUMAN **G** RecName: Full-Neuropeptide Y receptor type 2; Short=NPy2-R; AltName:  
 Full-NPY2 receptor; Short-Y2 receptor  
 gb|AAC50281.1| **G** neuropeptide Y/peptide YY Y2 receptor  
 gb|AAB04120.1| **G** neuropeptide yy2 receptor  
 gb|AAC51115.1| **G** type 2 neuropeptide Y receptor  
 gb|AA02062.1| **G** neuropeptide Y receptor Y2 [Homo sapiens]  
 gb|ANF75052.2| **G** Neuropeptide Y receptor Y2 [Homo sapiens]  
 gb|AAT75053.2| **G** Neuropeptide Y receptor Y2 [Homo sapiens]  
 gb|AYA04940.1| **G** unknown [Homo sapiens]  
 gb|EAX04901.1| **G** neuropeptide Y receptor Y2 [Homo sapiens]  
 Length=381

Gene ID: 4887 NPY2\_R | neuropeptide Y receptor Y2 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 167 bits (422), Expect = 9e-41, Method: Compositional matrix adjust.  
 Identities = 112/322 (34%), Positives = 164/322 (50%), Gaps = 23/322 (7%)  
 Query 42 VVAMFIVVAVLILPCLGNGVAVCFVVLVPPRERLTVRHFPIALAVSLPLAVGIV 101  
 Sbjct 49 I+AY I LL +GN+LV M TTV F1 NLAVL TL C+P TL VQVLLILAYCSIIILGVIGNSLVHIVVIIKFKSMRTVTFNFIANLA VADLLVN TLC LPLFT 108  
 Query 102 VDNLTGHPFDNATCPVAGQLGQVMSV+S+V S+V TL I+R RCIV+ + + R+ 161  
 Sbjct 109 TYTLMGBNWKGMPVLCIHPVPAVQGLAVQVOSTVITLTVTLADRHRCIVYHLESKIKRISFL 168  
 Query 162 IAVIVALIALLIMCPGSAVTLTVTREHHPW/DARNRSPVLYSCW+RNP - EKGRR-RVTT 218  
 Sbjct 169 IGLAWIGISALLA P+V S+V TL I+R RCIV+ + + C+ W P EX + VY+ 221  
 Query 219 VLFSHYIAPLAVIYVANIAKRLQCPGPAPGOGEEAADPFRSRR2RAVVMWLVWMLP 278  
 Sbjct 222 SLLILLYVPLGIIISPSYTRINSLKHNWPSG----AAMDHYHQRRQKTTTMLCVVVV 276  
 Query 279 FTLSWNPWLA VVALLLIDYQG - SLSQPLNHLVTVVYAFFPAHWLAFPN SANPIIYGYFNENF 336  
 Sbjct 277 F+SNLWPLA L +D L + L + F H +A ++ ANP+ +YG+ N N+ 332  
 Query 337 RRGPOAAFPARLPRPGSSHE 358  
 Sbjct 333 RKAFLGSAFRC-E-QRLDAHSE 352

>gb|AAA93170.1| G type 2 neuropeptide Y receptor  
Length=381

GENE ID: 4887 NPY2R | neuropeptide Y receptor Y2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 165 bits (417), Expect = 3e-40, Method: Compositional matrix adjust.  
Identities = 111/322 (34%), Positives = 163/322 (50%), Gaps = 23/322 (7%)

Query 42 VAAATIVAYALIPLLQCNVTLICFIVLJQRHNMHTVNNPFIILAVSLDLVVGICPOMPTTL 101  
V+ - I-AY I LL +-GN+LV +V+K + M TTVN FI NI-AV-DLVG C+P TL  
Sbjct 49 VGVVLILAYCSIIVLGVIGVNHVVIHVVKFKSMRTVTFNPFIIANLVAIDLVLVTPFLPTL 108

Query 102 VDNLLTGAWPPDNTAQMSGLVQGMSMVSASVFTLAVIAVERFCRIVHPFPREKLTLPLKALVT 161  
LT + W C + QG++ S T IA++RCIV+ K++ R +  
Sbjct 109 TTLYMEWGWMPGVLCIHLVYQGLAAQSTTITLTALEHRCIVVHBLSKISKRISPL 168

Query 162 IAVVIALALLIMCPAATVLTIVBEEHPPMVDAARNRSPLYSWCHEAMP---EKGRH-RVYTT 218  
I+ N + L+ P + L + RE + + + C E MP - EX + VY+  
Sbjct 169 IGLAWGISALLASP---LAIFPRYESLIEIIP---DPEIIVACTEKPGRGEKSIYOTVYSL 221

Query 219 VLFSHIYLPLALIIVMYARIKLCQAGPAPGOGREAAADPRASSRRAAVVVRHLVWALF 278  
+L+P+I+L+R+I+K+L+P+ AA +RR +MLV V+  
Sbjct 222 SLLLIVLPLGLGITSFVSPVQLKHNHVGPG-----AANDHYHQRQRKTTRMLVCVVVV 276

Query 279 FTLSWLPMLALLLIDVYQQ---LSAQPQHJLWTVYFAFPFAHMIAFPNNSANPIIYGFNFNF 336  
F+SWLPL A L +D + L + L+ P H +R + +ANP+Y+G- N +  
Sbjct 277 FAVSWLPLWAPQAVLDIDSQVLLDKEYKLI---FTVHIIAMCSTPANPLLYGMNSNRY 332

Query 337 RRGQAAARARLCPRPSSGSHKE 358  
R+ F +AFR C+P R+H E  
Sbjct 333 RKAFLSAFRC-E-QRLDAHSE 352

>ref|NP\_937822.2| G G protein-coupled receptor 103 [Homo sapiens]  
sp|Q96P65\_2| QRFP\_HUMAN | RecName: Full=Orxigenic neuropeptide QRFP receptor; AltName: Full=protein-coupled receptor 103; AltName: Full=SP93155;  
AltName: Full=R2Q27  
gb|EAX05262.1| G G protein-coupled receptor 103, isoform CRA\_b [Homo sapiens]  
Length=431

GENE ID: 84109 QRFP | pyroglutamylated RFamide peptide receptor [Homo sapiens]  
(10 or fewer Published links)

Score = 165 bits (417), Expect = 3e-40, Method: Compositional matrix adjust.  
Identities = 93/304 (30%), Positives = 159/304 (52%), Gaps = 21/304 (6%)

Query 51 ALIFLILQVNQNTLICFIVLJQRHNMHTVNNPFIILAVSLDLVVGICPOMPTTLVDNLGP 110  
LIF L + GN LV +V + + M TTVN FI -LA-SDL+ FC+P T+ N+ W  
Sbjct 53 VLGIALFALPGLVFTVYVTSRKSAMRTVTFNIFCISLALSDLLTTFCCIPVTMQLNISDNWL 112

Query 111 FINATCKMSGIVQGMSVSAASVFTLAVIAVERFCRIVHPFPREK---LTIAKALVITIAVIVAL 168  
CKR QV +V + T+ IAVER + +VHPF+ K - T R+A + V+W +  
Sbjct 113 GGATCCKMIVVPPVQSTAVTLELITNCIACVERHQGLVHPFKAKWQYTFRRAPTMZLWVWLV 172

Query 169 ALLINCP---SAVLTIVBEEHPPMVDAARNRSPLYSWCHEAMPKGMRHRVYTTLVFSHIYL 226  
A++ P L+ +F+ + + C E W + +VTT+ ++L  
Sbjct 173 AVIGVSPMVNHVQQLEI---KYDFLYKEHH----ICCLESWTSPVHQKITYTTLVILFL 224

Query 227 APALIIVVMYARIKLCQAGPANG-----GEAADPFRASRRARVWHMLVWALFP 279  
PL ++++++Y+I+L+ G +GE+ + +R+ + R+ M+ P  
Sbjct 225 LPMLVMLLILSYKIGEELWIKRKGDSVLRTHGKEM---KIAKKKKRAVIMMVTTVVALP 282

Query 280 TLSQLPLWALLLIDVYQOLSLPLHVTYAFFPAHNLAFPNSANPIIYGFNFNF 339  
+L+P+I+L+R+I+K+L+P+ AA +RR +MLV V+  
Sbjct 283 AVCAWPPPHVVIIDMIEYGSNPKEDDVTTKIMFIAVQIIGPSNSICNPVYPAHNFENPKXN 342

Query 340 FGQA 343  
Sbjct 343 VLSA 346

>dbj|BAC98938.1| G QRFP receptor [Homo sapiens]  
Length=431

GENE ID: 84109 QRFP | pyroglutamylated RFamide peptide receptor [Homo sapiens]  
(10 or fewer Published links)

Score = 164 bits (416), Expect = 4e-40, Method: Compositional matrix adjust.  
Identities = 93/304 (30%), Positives = 159/304 (52%), Gaps = 21/304 (6%)

Query 51 ALIFLILQVNQNTLICFIVLJQRHNMHTVNNPFIILAVSLDLVVGICPOMPTTLVDNLGP 110  
LIF L + GN LV +V + + M TTVN FI -LA-SDL+ FC+P T+ N+ W  
Sbjct 53 VLGIALFALPGLVFTVYVTSRKSAMRTVTFNIFCISLALSDLLTTFCCIPVTMQLNISDNWL 112

Query 111 FINATCKMSGIVQGMSVSAASVFTLAVIAVERFCRIVHPFPREK---LTIAKALVITIAVIVAL 168  
CKR QV +V + T+ IAVER + +VHPF+ K - T R+A + V+W +  
Sbjct 113 GGATCCKMIVVPPVQSTAVTLELITNCIACVERHQGLVHPFKAKWQYTFRRAPTMZLWVWLV 172

Query 169 ALLINCP---SAVLTIVBEEHPPMVDAARNRSPLYSWCHEAMPKGMRHRVYTTLVFSHIYL 226  
A++ P L+ +F+ + + C E W + +VTT+ ++L  
Sbjct 173 AVIGVSPMVNHVQQLEI---KYDFLYKEHH----ICCLESWTSPVHQKITYTTLVILFL 224

Query 227 APALIIVVMYARIKLCQAGPANG-----GEAADPFRASRRARVWHMLVWALFP 279  
PL ++++++Y+I+L+ G +GE+ + +R+ + R+ M+ P  
Sbjct 225 LPMLVMLLILSYKIGEELWIKRKGDSVLRTHGKEM---KIAKKKKRAVIMMVTTVVALP 282

Query 280 TLSQLPLWALLLIDVYQOLSLPLHVTYAFFPAHNLAFPNSANPIIYGFNFNF 339  
+L+P+I+L+R+I+K+L+P+ AA +RR +MLV V+  
Sbjct 283 AVCAWPPPHVVIIDMIEYGSNPKEDDVTTKIMFIAVQIIGPSNSICNPVYPAHNFENPKXN 342

Query 340 FGQA 343  
Sbjct 343 VLSA 346

```

>gb|[AAB07760.1] C neuropeptide Y/peptide Y receptor type 2
Length=381
GENE ID: 4887 NPY2R | neuropeptide Y receptor Y2 [Homo sapiens]
          (Over 10 PubMed links)

Score = 164 bits (414), Expect = 6e-40, Method: Compositional matrix adjust
Identities = 112/322 (34%), Positives = 163/322 (50%). Gaps = 23/322 (7%)
Query 42 VAAAMPYIAYALVLLPGLCNGVTLCPFCVFLVLRNHRMTVTFINFLIAASLDLVLGFCMPTTL 101
Sbjct 49 VVQVLLAYCISLLGVIGVNSLHVIIWVKPSHKTNFTVFIANLAVDVLNLVLCFLPFL 108
Query 102 VDNLLTGPMPFDNTKTCMGSGLVQOMSSVASVTFLLVIAVVERPCTVIFWHPRFVLLRKALVT 161
Sbjct 109 VVTTTGTGAGVPPVCLVHIVPVYQAGLVSQNSVTTILVTLAIDLRRKCIYVHLESRSKRISLPI 168
Query 162 IAVNALALLIICPMSPAVTLYTTERHHIPWDVADNRSPYPLSCWYMEW+- EKGRR--RVVTY 218
Sbjct 169 IGLGRIRSLALL- -LAIFPRYESLKLII-- DPFVLPCTKEWPAREKSIYGTGYVSL 221
Query 219 VLFSHTYLIVVLLVWYMAIRKLLQAGPARGGEAADRPSRRAKRVWVHMLWMAVLF 278
Sbjct 220 Y+ PD+ I Y RI KL P AA+ + M W V+ + MIV V+ + MIV V+ 278
Sbjct 222 SSSLVLLYVPLGQISFSPYTRWSKLWNSHVGSP-- AANDHYHORRKTTRKLVCVV 276
Query 279 FTSHLSLWLLALWLLIDYQG-- S-LAQJLWVTTTVAFFPAPMLAFNSNAMPIYGFNFEN 336
Sbjct 277 F+ SMLPL A L +D L + L + F H + A ++ ANP+Y+G N N+ 332
          FAVSNLHLQALPQ1DSDLKEYKKI-- FTVHIIAMCSFTPAFNLIGWMMNSH 332

Query 337 RRGQPAARFAFLCRPLPSSGSHKE 358
Sbjct 338 RRGQPAARFAFLCRPLPSSGSHKE 358

```

```
>ref|NP_000900.1| NPYR Human neuropeptide Y receptor Y1 [Homo sapiens]
sp|P25929.1|NPYR_HUMAN NPYR RecName: Full-Neuropeptide Y receptor type 1; AltName: Full-NPY-R
gb|AAAT7215.1| NPYR_HUMAN [Human neuropeptide Y peptide YY receptor mRNA, complete cds.], gene product
```



Sbjct 243 TFIILYILPLLLISVAYARAKKLWLCHNMGDVTTEQYFA --LRRKKKKTIKMLMLVVV 299

Query 278 FFTSLWLPWALLIDYQGQLAPQHLLVTVTVAFFPAHWLAFNNSAMPITIIGYFHNENFR 337  
 P L W PL +LL LS+ + F F HW A ++ NP IV + NENFR  
 Sbjct 300 LFALCFLPNCVYL --LSKVIRTNNALYPAF-HWFAMSSTCYNPFIYCHMLNENFR 353

Query 338 RGFQAAPRARLICPRPGSHKE 358  
 Sbjct 354 IELKALL--SMCQRPKPQED 372

>ref|NP\_057624.2| **G** G protein-coupled receptor 83 [Homo sapiens]  
 gb|ABY87919.1| **G** G protein-coupled receptor 83 [Homo sapiens]  
 Length=423

Gene ID: 10888 GPR83 | G protein-coupled receptor 83 [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 156 bits (395), Expect = 1e-37, Method: Compositional matrix adjust.  
 Identities = 105/321 (32%), Positives = 166/321 (51%), Gaps = 22/321 (6%)

Query 42 VAAAMPIVAYALIFLLCMVGNTLVCFIVLNRHMHTVNNPFLNLAVSDDLVGICFMPPTL 101  
 V A IVAY+ I + + GM LVC ++ EN+ MH+ T+PI+NLAV+D++ + P TL  
 Sbjct 70 VKALLIVAYSFIVLSPGNCVLCVHIFVQNRMSATSLSFVNLAVIDIMITLNLNTPTFL 129

Query 102 VDNLTGHPFDNATCNCMVGNTLVCFIVLNRHMHTVNNPFLNLAVSDDLVGICFMPPTL 161  
 V + + N F C+S Q S+ S TL ATAV+R + I+HP + ++++ K ++  
 Sbjct 130 VRVNSTWFGKNCVHSRAQYCSLHSVSAITLATAVDRHQV1MPLPKRPRISTKGVIY 189

Query 162 IAVINALLALIMCPSCAVTLVTREEHHPMDARNSYPLYSCWNEAMPKEG- MRRVYT 219  
 IAVIN+R P A+ + ++ RS C +PE +  
 Sbjct 190 IAVIN+TMATTPPSFLPHAIQKQLPFTKYS- EDIVRSL---CLDPDPPEPADLPWKYLDDA 242

Query 220 LPSHIYLAALIIVVMMYARAK- LQCAQPGPAGGEAADPRASRERRARVHMLMVVAL 277  
 F +Y+ PL +I + V YARA+AK LC G + + R+ + + + ML+V +  
 Sbjct 243 TFIILYILPLLLISVAYARAKKLWLCHNMGDVTTEQYFA --LRRKKKKTIKMLMLVVV 299

Query 278 FFTSLWLPWALLIDYQGQLAPQHLLVTVTVAFFPAHWLAFNNSAMPITIIGYFHNENFR 337  
 P L W PL +LL LS+ + F F HW A ++ NP IV + NENFR  
 Sbjct 300 LFALCFLPNCVYL --LSKVIRTNNALYPAF-HWFAMSSTCYNPFIYCHMLNENFR 353

Query 338 RGFQAAPRARLICPRPGSHKE 358  
 Sbjct 354 IELKALL--SMCQRPKPQED 372

>dbj|BA96064.1| **G** KIAA1540 protein [Homo sapiens]  
 Length=424

Gene ID: 10888 GPR83 | G protein-coupled receptor 83 [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 156 bits (395), Expect = 1e-37, Method: Compositional matrix adjust.  
 Identities = 105/321 (32%), Positives = 166/321 (51%), Gaps = 22/321 (6%)

Query 42 VAAAMPIVAYALIFLLCMVGNTLVCFIVLNRHMHTVNNPFLNLAVSDDLVGICFMPPTL 101  
 V A IVAY+ I + + GM LVC ++ EN+ MH+ T+PI+NLAV+D++ + P TL  
 Sbjct 71 VKALLIVAYSFIVLSPGNCVLCVHIFVQNRMSATSLSFVNLAVIDIMITLNLNTPTFL 130

Query 102 VDNLTGHPFDNATCNCMVGNTLVCFIVLNRHMHTVNNPFLNLAVSDDLVGICFMPPTL 161  
 V + + N F C+S Q S+ S TL ATAV+R + I+HP + ++++ K ++  
 Sbjct 131 VRVNSTWFGKNCVHSRAQYCSLHSVSAITLATAVDRHQV1MPLPKRPRISTKGVIY 190

Query 162 IAVINALLALIMCPSCAVTLVTREEHHPMDARNSYPLYSCWNEAMPKEG- MRRVYT 219  
 IAVIN+R P A+ + ++ RS C +PE +  
 Sbjct 191 IAVIN+TMATTPPSFLPHAIQKQLPFTKYS- EDIVRSL---CLDPDPPEPADLPWKYLDDA 243

Query 220 LPSHIYLAALIIVVMMYARAK- LQCAQPGPAGGEAADPRASRERRARVHMLMVVAL 277  
 F +Y+ PL +I + V YARA+AK LC G + + R+ + + + ML+V +  
 Sbjct 244 TFIILYILPLLLISVAYARAKKLWLCHNMGDVTTEQYFA --LRRKKKKTIKMLMLVVV 300

Query 278 FFTSLWLPWALLIDYQGQLAPQHLLVTVTVAFFPAHWLAFNNSAMPITIIGYFHNENFR 337  
 P L W PL +LL LS+ + F F HW A ++ NP IV + NENFR  
 Sbjct 301 LFALCFLPNCVYL --LSKVIRTNNALYPAF-HWFAMSSTCYNPFIYCHMLNENFR 354

Query 338 RGFQAAPRARLICPRPGSHKE 358  
 Sbjct 355 IELKALL--SMCQRPKPQED 373

>gb|AAH67474.1| **G** G protein-coupled receptor 83 [Homo sapiens]  
 Length=423

Gene ID: 10888 GPR83 | G protein-coupled receptor 83 [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 152 bits (385), Expect = 2e-36, Method: Compositional matrix adjust.  
 Identities = 103/321 (32%), Positives = 166/321 (51%), Gaps = 22/321 (6%)

Query 42 VAAAMPIVAYALIFLLCMVGNTLVCFIVLNRHMHTVNNPFLNLAVSDDLVGICFMPPTL 101  
 V A IVAY+ I + + GM LVC ++ EN+ MH+ T+PI+NLAV+D++ + P TL  
 Sbjct 70 VKALLIVAYSFIVLSPGNCVLCVHIFVQNRMSATSLSFVNLAVIDIMITLNLNTPTFL 129

Query 102 VDNLTGHPFDNATCNCMVGNTLVCFIVLNRHMHTVNNPFLNLAVSDDLVGICFMPPTL 161  
 V + + N F C+S Q S+ S TL ATAV+R + I+HP + ++++ K ++  
 Sbjct 130 VRVNSTWFGKNCVHSRAQYCSLHSVSAITLATAVDRHQV1MPLPKRPRISTKGVIY 189

Query 162 IAVINALLALIMCPSCAVTLVTREEHHPMDARNSYPLYSCWNEAMPKEG- MRRVYT 219  
 IAVIN+R P A+ + ++ RS C +PE +  
 Sbjct 190 IAVIN+TMATTPPSFLPHAIQKQLPFTKYS- EDIVRSL---CLDPDPPEPADLPWKYLDDA 242

Query 220 LPSHIYLAALIIVVMMYARAK- LQCAQPGPAGGEAADPRASRERRARVHMLMVVAL 277  
 F +Y+ PL +I + V YARA+AK LC G + + R+ + + + ML+V +  
 Sbjct 243 TFIILYILPLLLISVAYARAKKLWLCHNMGDVTTEQYFA --LRRKKKKTIKMLMLVVV 299

Query 278 FFTSLWLPWALLIDYQGQLAPQHLLVTVTVAFFPAHWLAFNNSAMPITIIGYFHNENFR 337  
 P L W PL +LL LS+ + F F HW A ++ NP IV + NENFR

Sbjct 300 L<sup>+</sup>FALCWPLN<sup>Y</sup>VLL----LSSK<sup>W</sup>IRTNNA<sup>Y</sup>FAF-HWFAMS<sup>ST</sup>CYNP<sup>Y</sup>FCWLN<sup>N</sup>FR 353

Query 338 RG<sup>Q</sup>QAA<sup>R</sup>ARL<sup>L</sup>CP<sup>R</sup>PG<sup>S</sup>SH<sup>K</sup>E 358

Sbjct 354 IELMALL--SNCQR<sup>P</sup>PKPQED 372

>gb|AAI28134.1| GPR103 protein [Homo sapiens]  
Length=356

Gene ID: 84109 QRFPRK | pyroglutamylated RFamide peptide receptor [Homo sapiens]  
(10 or fewer PubMed links)

Score = 149 bits (375), Expect = 2e-15, Method: Compositional matrix adjust.  
Identities = 84/281 (29%), Positives = 144/281 (51%), Gap = 21/281 (7%)

Query 74 MHTVTRRNPFLAVSLDVLW<sup>+</sup>GICMP<sup>Y</sup>TFVNL<sup>+</sup>LTGMPFDNATC<sup>Y</sup>QSGLW<sup>+</sup>QNS<sup>Y</sup>VEASVPT 133

Sbjct 1 MRTVTRN<sup>Y</sup>FLAVSLDVLW<sup>+</sup>GICMP<sup>Y</sup>TFVNL<sup>+</sup>LTGMPFDNATC<sup>Y</sup>QSGLW<sup>+</sup>QNS<sup>Y</sup>VEASVPT 60

Query 134 LVAIAVERP<sup>R</sup>CFIVHP<sup>P</sup>RFK<sup>Y</sup>--L<sup>+</sup>TRAKA<sup>Y</sup>W<sup>+</sup>TAVI<sup>Y</sup>W<sup>+</sup>TA<sup>Y</sup>LL<sup>+</sup>IMCP<sup>Y</sup>--SAVLT<sup>Y</sup>TVREBHF 189

Sbjct 61 MTCIAVERRH<sup>Y</sup>QGLVHP<sup>P</sup>FM<sup>Y</sup>W<sup>+</sup>TRAP<sup>R</sup>TFV<sup>Y</sup>GVMV<sup>Y</sup>HLAVAV<sup>Y</sup>GS<sup>Y</sup>PM<sup>Y</sup>W<sup>+</sup>QOLEI<sup>Y</sup>--KYDF 117

Query 190 NMDARNR<sup>Y</sup>SPLYPS<sup>W</sup>CEAM<sup>Y</sup>PEKGM<sup>Y</sup>RRV<sup>Y</sup>TTT<sup>Y</sup>V<sup>Y</sup>FSH<sup>Y</sup>YL<sup>Y</sup>PLA<sup>Y</sup>LL<sup>Y</sup>LV<sup>Y</sup>W<sup>Y</sup>Y<sup>Y</sup>ARI<sup>Y</sup>AKR<sup>Y</sup>Q<sup>Y</sup>AGP<sup>Y</sup> 249

Sbjct 118 NY<sup>Y</sup>KE<sup>Y</sup>---ICCLEBMT<sup>Y</sup>SPH<sup>Y</sup>W<sup>Y</sup>H<sup>Y</sup>TF<sup>Y</sup>PLV<sup>Y</sup>LL<sup>Y</sup>PLW<sup>Y</sup>ML<sup>Y</sup>LL<sup>Y</sup>SKY<sup>Y</sup>EL<sup>Y</sup>W<sup>Y</sup>KERV 172

Query 250 AG<sup>Y</sup>---GE<sup>Y</sup>PA<sup>Y</sup>ND<sup>Y</sup>PR<sup>Y</sup>AS<sup>Y</sup>RA<sup>Y</sup>RV<sup>Y</sup>HM<sup>Y</sup>U<sup>Y</sup>W<sup>Y</sup>LP<sup>Y</sup>TL<sup>Y</sup>SH<sup>Y</sup>LP<sup>Y</sup>W<sup>Y</sup>LL<sup>Y</sup>LL<sup>Y</sup>D<sup>Y</sup>Y<sup>Y</sup>GQL<sup>Y</sup>SA<sup>Y</sup> 302

Sbjct 173 GDGSVL<sup>Y</sup>LT<sup>Y</sup>HG<sup>Y</sup>KEM<sup>Y</sup>--X<sup>Y</sup>AKR<sup>Y</sup>KK<sup>Y</sup>RA<sup>Y</sup>VI<sup>Y</sup>M<sup>Y</sup>NT<sup>Y</sup>TV<sup>Y</sup>VAL<sup>Y</sup>F<sup>Y</sup>AVC<sup>Y</sup>W<sup>Y</sup>HP<sup>Y</sup>V<sup>Y</sup>HH<sup>Y</sup>MI<sup>Y</sup>EY<sup>Y</sup>SN<sup>Y</sup>KEY 230

Query 303 IHL<sup>Y</sup>LV<sup>Y</sup>TV<sup>Y</sup>APP<sup>Y</sup>FA<sup>Y</sup>HLA<sup>Y</sup>PL<sup>Y</sup>PN<sup>Y</sup>SAN<sup>Y</sup>PI<sup>Y</sup>GY<sup>Y</sup>FN<sup>Y</sup>EN<sup>Y</sup>PR<sup>Y</sup>QQA<sup>Y</sup> 343

Sbjct 231 DDDT<sup>Y</sup>IKM<sup>Y</sup>IFI<sup>Y</sup>AI<sup>Y</sup>QI<sup>Y</sup>GS<sup>Y</sup>NS<sup>Y</sup>ICN<sup>Y</sup>PI<sup>Y</sup>VV<sup>Y</sup>AF<sup>Y</sup>PM<sup>Y</sup>NN<sup>Y</sup>FK<sup>Y</sup>NN<sup>Y</sup>SSA 271

>ref|NP\_003848.1| GPR103 galanin receptor 2 [Homo sapiens]

sp|043603.1| GALR2\_HUMAN GPR103 galanin receptor type 2; AltName: Full=GAL2-R;

AltName: Full=GALR2

gb|AAC39634.1| GPR103 galanin receptor GalR2 [Homo sapiens]

10 more sequence titles

gb|AAC18118.1| GPR103 galanin receptor subtype 2 [Homo sapiens]

gb|AAC36587.1| GPR103 galanin receptor type 2 [Homo sapiens]

gb|AAD08671.1| GPR103 galanin receptor type 2 [Homo sapiens]

gb|AAH69130.1| GPR103 galanin receptor 2 [Homo sapiens]

gb|AAH74914.1| GPR103 galanin receptor 2 [Homo sapiens]

gb|AAH74915.1| GPR103 galanin receptor 2 [Homo sapiens]

gb|AAI09053.1| GPR103 galanin receptor 2 [Homo sapiens]

gb|AAI09052.1| GPR103 galanin receptor 2 [Homo sapiens]

gb|AAW9364.1| GPR103 galanin receptor 2 [Homo sapiens]

gb|ABQ52421.1| GPR103 galanin receptor 2 [Homo sapiens]

Length=387

Gene ID: 8811 GALR2 | galanin receptor 2 [Homo sapiens] (Over 10 PubMed links)

Score = 148 bits (374), Expect = 3e-15, Method: Compositional matrix adjust.  
Identities = 122/373 (32%), Positives = 181/373 (48%), Gap = 42/373 (11%)

Query 41 P<sup>Y</sup>AMP<sup>Y</sup>IV<sup>Y</sup>AY<sup>Y</sup>AL<sup>Y</sup>LI<sup>Y</sup>PL<sup>Y</sup>LC<sup>Y</sup>W<sup>Y</sup>NT<sup>Y</sup>FC<sup>Y</sup>IV<sup>Y</sup>PL<sup>Y</sup>W<sup>Y</sup>NR<sup>Y</sup>HM<sup>Y</sup>TF<sup>Y</sup>N<sup>Y</sup>MP<sup>Y</sup>FL<sup>Y</sup>A<sup>Y</sup>SD<sup>Y</sup>LL<sup>Y</sup>W<sup>Y</sup>GF<sup>Y</sup>CM<sup>Y</sup>PT<sup>Y</sup> 100

Sbjct 23 PEAVIV<sup>Y</sup>PL<sup>Y</sup>FA<sup>Y</sup>I<sup>Y</sup>PL<sup>Y</sup>W<sup>Y</sup>GT<sup>Y</sup>VG<sup>Y</sup>TL<sup>Y</sup>LA<sup>Y</sup>VL<sup>Y</sup>RL<sup>Y</sup>GC<sup>Y</sup>Q<sup>Y</sup>VS<sup>Y</sup>ST<sup>Y</sup>TM<sup>Y</sup>FL<sup>Y</sup>IM<sup>Y</sup>GV<sup>Y</sup>AD<sup>Y</sup>LC<sup>Y</sup>FL<sup>Y</sup>CC<sup>Y</sup>PF<sup>Y</sup>Q 82

Query 101 LDVNL<sup>Y</sup>ITG<sup>Y</sup>MP<sup>Y</sup>FL<sup>Y</sup>ATC<sup>Y</sup>W<sup>Y</sup>QGMS<sup>Y</sup>SV<sup>Y</sup>AS<sup>Y</sup>SV<sup>Y</sup>PT<sup>Y</sup>LA<sup>Y</sup>IV<sup>Y</sup>ER<sup>Y</sup>PR<sup>Y</sup>CF<sup>Y</sup>HF<sup>Y</sup>--REKU<sup>Y</sup>TL<sup>Y</sup>RA<sup>Y</sup> 158

Sbjct 83 ATIV<sup>Y</sup>TYL<sup>Y</sup>LG<sup>Y</sup>W<sup>Y</sup>FG<sup>Y</sup>SL<sup>Y</sup>CKA<sup>Y</sup>HL<sup>Y</sup>FL<sup>Y</sup>PT<sup>Y</sup>IN<sup>Y</sup>W<sup>Y</sup>ASS<sup>Y</sup>FT<sup>Y</sup>LA<sup>Y</sup>VS<sup>Y</sup>DL<sup>Y</sup>Y<sup>Y</sup>LA<sup>Y</sup>RY<sup>Y</sup>PL<sup>Y</sup>HS<sup>Y</sup>REL<sup>Y</sup>TP<sup>Y</sup>TR<sup>Y</sup> 142

Query 159 LT<sup>Y</sup>IV<sup>Y</sup>TA<sup>Y</sup>LA<sup>Y</sup>LL<sup>Y</sup>IMCP<sup>Y</sup>SV<sup>Y</sup>TT<sup>Y</sup>Y<sup>Y</sup>TR<sup>Y</sup>EE<sup>Y</sup>W<sup>Y</sup>H<sup>Y</sup>MD<sup>Y</sup>DA<sup>Y</sup>RS<sup>Y</sup>PL<sup>Y</sup>Y<sup>Y</sup>SC<sup>Y</sup>NE<sup>Y</sup>AM<sup>Y</sup>PE<sup>Y</sup>KG<sup>Y</sup>MR<sup>Y</sup>VT<sup>Y</sup> 218

Sbjct 143 L<sup>+</sup>TA<sup>Y</sup>IGL<sup>Y</sup>LA<sup>Y</sup>PL<sup>Y</sup>LS<sup>Y</sup>LS<sup>Y</sup>FG<sup>Y</sup>----P<sup>+</sup>Y<sup>Y</sup>LS<sup>Y</sup>TY<sup>Y</sup>YY<sup>Y</sup>-----SOL<sup>Y</sup>Q<sup>Y</sup>LT<sup>Y</sup>CP<sup>Y</sup>W<sup>Y</sup>AP<sup>Y</sup>RR<sup>Y</sup>RR<sup>Y</sup>MD<sup>Y</sup>MI<sup>Y</sup> 169

Query 219 VLF<sup>Y</sup>SH<sup>Y</sup>YL<sup>Y</sup>LA<sup>Y</sup>PL<sup>Y</sup>AL<sup>Y</sup>IV<sup>Y</sup>Y<sup>Y</sup>Y<sup>Y</sup>AR<sup>Y</sup>Y<sup>Y</sup>RL<sup>Y</sup>QC<sup>Y</sup>A<sup>Y</sup>PG<sup>Y</sup>GE<sup>Y</sup>AA<sup>Y</sup>PR<sup>Y</sup>SR<sup>Y</sup>RR<sup>Y</sup>AR<sup>Y</sup>Y<sup>Y</sup>BN<sup>Y</sup>W<sup>Y</sup>MF<sup>Y</sup>AL<sup>Y</sup>VF<sup>Y</sup> 278

Sbjct 190 F<sup>Y</sup>YL<sup>Y</sup>P<sup>+</sup>Y<sup>Y</sup>Y<sup>Y</sup>AR<sup>Y</sup>Y<sup>Y</sup>RL<sup>Y</sup>QC<sup>Y</sup>A<sup>Y</sup>PG<sup>Y</sup>GE<sup>Y</sup>AA<sup>Y</sup>PR<sup>Y</sup>SR<sup>Y</sup>RR<sup>Y</sup>AR<sup>Y</sup>Y<sup>Y</sup>BN<sup>Y</sup>W<sup>Y</sup>MF<sup>Y</sup>AL<sup>Y</sup>VF<sup>Y</sup> 244

Query 279 FTLSL<sup>Y</sup>PL<sup>Y</sup>W<sup>Y</sup>LL<sup>Y</sup>LL<sup>Y</sup>LL<sup>Y</sup>YDQ<sup>Y</sup>QL<sup>Y</sup>HL<sup>Y</sup>W<sup>Y</sup>TY<sup>Y</sup>APP<sup>Y</sup>--FA<sup>Y</sup>HM<sup>Y</sup>LA<sup>Y</sup>FF<sup>Y</sup>NS<sup>Y</sup>AN<sup>Y</sup>PI<sup>Y</sup>II<sup>Y</sup>Y<sup>Y</sup>GF<sup>Y</sup>HE<sup>Y</sup>PR<sup>Y</sup> 337

Sbjct 245 F<sup>Y</sup>LC<sup>Y</sup>LM<sup>Y</sup>PH<sup>Y</sup>HAL<sup>Y</sup>LL<sup>Y</sup>CV<sup>Y</sup>MF<sup>Y</sup>Q<sup>Y</sup>FL<sup>Y</sup>TR<sup>Y</sup>-----Y<sup>Y</sup>A<sup>Y</sup>LA<sup>Y</sup>LL<sup>Y</sup>SH<sup>Y</sup>Y<sup>Y</sup>TS<sup>Y</sup>AN<sup>Y</sup>SC<sup>Y</sup>VC<sup>Y</sup>NP<sup>Y</sup>IV<sup>Y</sup>VAL<sup>Y</sup>VS<sup>Y</sup>EH<sup>Y</sup>K<sup>Y</sup> 300

Query 338 RGF<sup>Y</sup>-----QAFRA<sup>Y</sup>--RLCP<sup>Y</sup>PR<sup>Y</sup>SG<sup>Y</sup>SH<sup>Y</sup>KE<sup>Y</sup>Y<sup>Y</sup>SER<sup>Y</sup>RP<sup>Y</sup>GG<sup>Y</sup>--LL<sup>Y</sup>-R<sup>Y</sup>RF<sup>Y</sup>V<sup>Y</sup>V<sup>Y</sup>R<sup>Y</sup>PS<sup>Y</sup>D<sup>Y</sup>SL<sup>Y</sup>GP<sup>Y</sup> 384

Sbjct 301 KOFRTICAG<sup>Y</sup>IL<sup>Y</sup>GR<sup>Y</sup>AP<sup>Y</sup>GR<sup>Y</sup>AS<sup>Y</sup>RV<sup>Y</sup>CA<sup>Y</sup>ARG<sup>Y</sup>TH<sup>Y</sup>GS<sup>Y</sup>VL<sup>Y</sup>RE<sup>Y</sup>ESS<sup>Y</sup>D<sup>Y</sup>LL<sup>Y</sup>HM<sup>Y</sup>SE<sup>Y</sup>AG<sup>Y</sup>AL<sup>Y</sup>RPC<sup>Y</sup>---P 356

Query 385 S<sup>Y</sup>SEGP<sup>Y</sup>SS<sup>Y</sup>GA<sup>Y</sup>PR<sup>Y</sup>RG<sup>Y</sup> 397

S<sup>Y</sup> P<sup>Y</sup> P<sup>Y</sup> PG<sup>Y</sup> 369

>gb|AAB05897.1| GPR103 neurokinin-2 receptor

Length=398

Gene ID: 6865 TACR2 | tachykinin receptor 2 [Homo sapiens]

(Over 10 PubMed links)

Score = 146 bits (373), Expect = 4e-35, Method: Compositional matrix adjust.  
Identities = 117/408 (28%), Positives = 185/408 (45%), Gap = 25/408 (6%)

Query 21 N<sup>+</sup>TEAT<sup>Y</sup>PAT<sup>Y</sup>NL<sup>Y</sup>TT<sup>Y</sup>Y<sup>Y</sup>TS<sup>Y</sup>YY<sup>Y</sup>QNT<sup>Y</sup>PS<sup>Y</sup>VA<sup>Y</sup>MT<sup>Y</sup>IV<sup>Y</sup>Y<sup>Y</sup>AR<sup>Y</sup>Y<sup>Y</sup>PL<sup>Y</sup>FL<sup>Y</sup>CM<sup>Y</sup>GN<sup>Y</sup>TL<sup>Y</sup>FC<sup>Y</sup>IV<sup>Y</sup>PL<sup>Y</sup>W<sup>Y</sup>NR<sup>Y</sup>HM<sup>Y</sup>TV<sup>Y</sup>TN<sup>Y</sup> 80

Sbjct	11	NISSGESPNTTGTAFSNPSQLMAYLALVLVATGNAIVINIIILAHRRMRTVTNY	70
Query	81	FILNALVSUDLJWUFGCMMPTTFLNLTGWPFDNATCMQSLWVGQNSVASASVTFVVAIE FI-FL-NA-+D + P F V H F A C L S + S++ + AIA +	140
Sbjct	71	FIVLNAEMLCAHNPAAFHNFYVASHNWFYGRGAFLPPIFTAMHNSMTAIAAD	130
Query	141	RFC1VHPFPPEKRLVTLRKEALVATIIMALVNCMPSTVLTLYTREEHHPW/DARNRSYPL R+ I VHPFP +L+ A+ JN + AL + P T VT +	200
Sbjct	131	RYMAVHFVPPFLPSAFKSTVAGIMWLVALASLACOFCPYSTMD-----GA	178
Query	201	YSCNEAPMKGMR-----VYTWTUFLSHYLALAPLWVYMYARIAHLQCGAPPLPGEEA C AMPE + B + Y I PLAA+V Y Y I L + P G + A	256
Sbjct	179	TCKVUAWPDEGSKTLLYHLLWVIALIYFLVPLAQMVGATVYLSHJLRRMAPP-----GGQA	235
Query	257	-ADPRASERRARVHVHLWVMLPFLSMLWPLAWLILLIYDQQLSAPQHLHJWVTVYAFFAH A+ R + ++ V + V+L F + WLP + L+ + + + V + V F	255
Sbjct	236	GANLRLHJAKKFFVKTMVTHFATLICMFLYHLYFLIGSPEOYICHKIQVYQYLALF-----	293
Query	316	MIAFPNSANPAIYGVNENPRPGQAAFPARLCRPRGSSHIIAEYERPGPGLHLHRVVFV MIA + + NPIIY R FR GPF AP CP + + + P L V R	375
Sbjct	294	NLMASSTWYHNPVYIICLNHLHRFRSGSFLLAFLRC - CPTCCEKELLELTPLSTLSTRVNRC	351
Query	376	PRTPSGSLPSSGSPSSGAPGRPLPQJLNGRVAHNHLRPGCQPSHLR	423
Sbjct	352	+ PS P + G P + H +	398
Query	352	HTKETLPNLAGDTWPSATSEASCEAGR+ QDGSGLMFGYCLLAPTTKTHVE	398

>gb|M3H99637.1| G Pancreatic polypeptide receptor 1 [Homo sapiens]

Length=375

GENE ID: 5540 PPYR1 | pancreatic polypeptide receptor 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 148 bits (373), Expect = 4e-35, Method: Compositional matrix adjust.  
Identities = 103/336 (30%), Positives = 166/336 (49%), Gaps = 19/336 (5%)

```

Query 14 PLSQLNTNTATPATNLTFSYYQHTSPVAAMPIVAYALIFLICMVGNLVCFIVLKNRH 73
P S G N T F S + Q + V + +Y++ + + +GN + + + + +
Sbjctn 14 PNSGNTNTATPATNLTFSYYQHTSPVAAMPIVAYALIFLICMVGNLVCFIVLKNRH 73

```

Query 74 MHTVTNMFIILNLAVS DLLV GICM PTTL VDN LITG WPF DNATCK MSG LVQ GM VSAS VFT 133

Sbjct 72 KANVTNLIANLAFPSDPLMCLLCQPLTAVY蒂MDYWIPGETLCKMSAFIQCMCSVTSILS 131  
GUNNAR 124 LUNINVERPGLHEDREKLTDEKLWLTIRHMLILLIMCD--SRVNTTHEBKK-- 137

Sbjct 132 LV+A+ER + I++P K ++ +A + I +IW +A ++ P +++ V + H  
LVLVALERHQLIINPTGWNKPSISQAYLGIVLIACVLSLPFLANSILENVPFHKNHSA 191

```

Query 188 -HFMVDARNRSYPLYSWCEAWPEKGMRVYTTVLFSHIYLAPLALIVUVMYARIARKLCQA 246
          F+ D           C E+WP   R+ TTY L   Y PL I+V YARI R+L Q
Subject 182 TPLAFLADK 1MPCGCDW1KJHJF1W1T1L1D1O1C1D1G1I1V1A1R1D1P1Q1 243

```

Query 247 PGPAPGGERAADPRASRRRARVHMLVMVALFTTLSWLPWLALLLIDYQQLSAPQLHLV 306

Query 302 TIVAFRERAHWLSSEENSSANDIIVCYVENENEEPRGEQD 342

Sbjct 302 LI--FLVCHLLAMASTCVNPPIYGFLNTNFKKEIKA 335

>ref|NP\_000721.1| **UG** cholecystokinin A receptor [Homo sapiens]

sp|P32238.1|CCRAR\_HUMAN RecName: Full=Cholecystokinin receptor type A; Al receptor; Short=CCK-AR; AltName: Full=Cholecystokinin-1

gb|AAA35659.1| C cholecystokinin A receptor  
3 more reference titles

gb|AAA02819.1| G cholecystokinin A receptor

gb|AAA91123.1| G cholecystokinin type A receptor  
gb|PAN0879.1| G cholecystokinin type-A receptor [ Homo sapiens ]

gb|NP84362.1| G cholecystokinin A receptor [Homo sapiens]

gb|EAW92850.1| C cholecystokinin A receptor [Homo sapiens]

dbj|BAG36692.1| unnamed protein product (Homo sapiens)  
Length=428

GENE ID: 886 CCKAR | cholecystokinin A receptor (Homo sapiens)  
(Over 10 PubMed links)

Score = 147 bits (370), Expect = 8e-35, Method: Compositional matrix adjust  
Identities = 109/353 (30%), Positives = 173/353 (49%), Gaps = 61/353 (17%)

Sbjct 102 NLLKDP1PGSAVCKTTTFMGTTSVSVSTFNLVAISLERYGAICKPLQSRVWQTKSALKV 161

Query 162 IAATWCLSLIMCPASVAVLIVIREEHHFMDKRSVPLISCHSWPESRGRMRRVTFDP 221  
IA W L+ IM P + + + +N + C P M++ + T L  
Sbjct 162 IAATWCLSLIMTPYPI-----YSNLVPFTKNNNOTANMCRFLLPNDVMOQSWHTFLL 214

Query 222 SHIYLAPLALIVVMMYARIARKLCQA-----PGPAPGGE-RAAD----- 258  
++L P +++V Y I+ +L Q P G+ E +D

```

Subject 215 LILFLIPGVMMVAYGLISLELYQGIRPEASQKSAKERKPSTTSSGKYEDSDGCYLQKT 274
Query 259 -----PRASRRRA----- RVVHMLVMVALPFTLSQLPLNALL 291

```

Sbjct 275 RPPRKLELRQLSTGSSSRANRIRSNSSAANILMAKKRVIRMLIVIVVLFLCWMPIFSANA 334

Query 292 LIDYQQLSAPQLHLVTYAFPPFAHWLIAFFNNSANPIIYGFNNFRGRGFAQAF 344  
Y SA + + F LL + S NPII + N + FR GF A F  
Sbjct 335 WRAYDTASAER--RLSGTPISFILLSSYTSSCVNPICYCFMNRKFRGLGMATF 385

```
>sp|P21452|2_NKR_HUMAN [G] RecName: Full=Substance-K receptor; Short=SKR; AltName: Full=Neurokinin A receptor; Location: Null; NK-2 receptor; Short=NK-2R; AltName: Full=neurokinin receptor 2  
gb|[AB20303_1] [G] neurokinin-2 receptor, NK-2 receptor [human, Peptide, 398 aa]  
gb|[AP04358_1] [G] tachykinin receptor 2 [Homo sapiens]  
gb|[BAW54324_1] [G] tachykinin receptor 2, isoform CRA_a [Homo sapiens]  
dbj|[BAP84685_1] [G] unnamed protein product [Homo sapiens]  
Length=398
```

GENE ID: 6865 TACR2 | tachykinin receptor 2 (Homo sapiens)  
(Over 10 PubMed links)

Score = 146 bits (369), Expect = 1e-34, Method: Compositional matrix adjust.  
Identities = 117/408 (28%), Positives = 184/408 (45%), Gaps = 25/408 (6%)

Query	21	NTEATPATNLTFTSSYYQTPVAAFMIVAYALIFPLLCMVNGUWLCFV1LKHRRHMHTVTNM	80
N	+ P + N T + + S	R++ AY + L+ + GN -v + I+ L + R M TVIN	
Sbjct	11	NISSGPESNITGTIAFSMPSWQLNLAWTAYALLVAVTGNAIVIWIILAHRRMRTVINY	70

Query	81	FILNLALSVSDDLVGIFCPMTTLVWDLNLTGWPFDNATCKMSLVLQGMSVSASVFTLVAIVE	140
		FI+LA+++DL + F V W P A C L + + S +++ AIA +	
Sbjct	71	FIVNLALADLCMAAPNAFPNVYASHNIWYFGRAFCYFQNLLPITAMFVSIYSMTAIAAD	130

Query 141 RFRCPHPPREKLTRKALVIAWILALIMCPASVLTIVTRBEHHFMVDARNRSYPL 200  
R+ IVHPFP+ +L IA IW +AL + P TVT ++  
Sbjct 131 RYMAIVHPFPQRLSAPSTKAVIAGINLVALALASPOCFYSTVMDQ ----- GA 178

Sbjct 294 WLA ++ NPIIY N FR GF+ AFR CP + + + P L RV  
WLAMSTHNYVIIYCCLNHRFRGCFRLAFCR - CPWVTPTKDEQKLELPTTLSSTRVNRC 351  
Query 376 VRPSDGSQPLSPRSGPSSGAPEPGRLPLRNGRVIAHHGLPRRGPGCSHLPL 423

Sbjct 352 HTKETLFBAGDTAPSEATSGEAGR P-QDGSCLWFGYGLLAFTKTHVBI 398

gb|AAA60347.1| G neurokinin A receptor  
Length=398

GENE ID: 6865 TACR2 | tachykinin receptor

Queso I.B. (Over 10 Pounds)

Score = 145 bits (366) Expect = 28-34 Method: Composit

Score = 145 bits (366), Expect = 3e-34, Method: Compositional matrix  
Identities = 117/408 (28%), Positives = 184/408 (45%), Gaps = 25/408 (

Query 21	NTEATPNTLTFSSYYQHSPAMVIFAYALIPPLCLMVGNTLVCFIVLNLRRHMVTVN	80
N + P +N T + * S A++ AY + L+ G + V + R + M TVTN		
Sbjct 11	NISSGPESNTTGTITAFSPMSWPQLALWAPAYLALVLVAVTGNAIVIWIILAHRRMRVTNY	70

Query 61 FILNLALADLWGFPMFLVLLGFLNGLFVNACAGSRLVQGMVSASPTFLVAVR 140  
FT+NL+A+DL + F V W P A C L ++ S+++ AIA +  
Sbjct 71 FIVNLALADLCMAAFNAFPNFVYASHNNIWyGRACYFQNLFPPITAMFVSIYSMTAIAAD 130

Subjct 179 C ANPE + + Y V+ + YY PLA+ V Y+ I L + P G +A  
 TKCVVANPDRGGKTIIJLHVVITAIYFLPLAVMFVAYSVTIGITIWRRAVP--GHQHA 235  
 Questy 257 -ADFRASBRAPPVHMLVMALFETISWLPLWALLIDYGOALSAPOLHIVTVYDFFPAH 315

Sbjct	236	A+ R + + + V + V L F + WLP + L + + + + VY F GANHLRQLQKPFVKTMLVLUVLTFAICWLPHLYLFLGSDPEIYCHKFQIOVYLFLL--	293
Query	316	WLAFFNSSLANPIIYGFNFENFRGFOAFAFRARLCPRPSGHKEAYSERPGGLLHRRVFVV	375

Sbjct 294 WLA ++ NPIIY N FR GF+ AFR CP + + + P L RV  
WLAMSTNMYNIIYCCNLNR FRSQGFLAFRC - CPWVPTKCFKLLEPTTSLSRVNRC 351  
Query 376 VRPSDSGLPSESGPSSGAPRPGRLPLRNGRVAHHGLPREPGPCSHLPL 423

Sbjct 352 HTKETLPMAGDTAPSEATSGEAGRP-QDGSGLWFGYGLLAPTKTHVIEI 398

>ref|NP\_005963.3| pancreatic polypeptide receptor 1 [Homo sapiens]  
sp|P50391.1|NPY4R\_HUMAN G RecName: Full=Neuropeptide Y receptor type 4; Short=Pancreatic polypeptide receptor 1; Short=PPI1

gb|AAC50280.1| G neuropeptide Y4 receptor protein  
emb|CAA91433.1| G pancreatic polypeptide receptor PPL [Homo sapiens]  
-|AB22220.1| G pancreatic polypeptide receptor 1 [Homo sapiens]

emb|CAI13318.1| G pancreatic polypeptide receptor 1 [Homo sapiens]  
gb|AAVE68197.1| G pancreatic polypeptide receptor 1 [Homo sapiens]  
Length=375

Score = 145 bits (366), Expect = 3e-34, Method: Compositional matrix adjust.  
Identities = 103/336 (30%), Positives = 167/336 (49%), Gaps = 19/336 (5%)

Query 14 PLSQNGTNTTEATPATHTNFTSSYYQHTSPVAAAMPFIVAYALIPLLCMVGNHTLVCFLVJLQRNH 73  
P S G N T F PS + O V + \*++ + \*+\* ++ +GN + \*++ +  
Sbjct 12 PKSPOGENRSKPLGTYPNFNSCQSDVWDVNVFIVTYSIETVVGLVGLNLICMCTVTRQNE 71  
Query 74 MHTVTINMPFIANLAWSDLWLGIFCMPTTLVONLITGMPFDNATCNCMGLVQGMGSVASVFT 133  
VTN+ I NLA SD L+ C P T V + + M F CMKS +O MSV+ S+  
Sbjct 72 KANVNLJIANLAFAFSDFMLCQLQPIVATVYDYMWIGETLCKMSAFIQCSMSVTVSILS 131  
Query 134 LVIAIAVERFCIVHPFREKLRLKAVALTIAVIMALALLIMCP---SAVLTUTVREHE--- 187  
LV+A+ER+ +I+P+ K ++ +A + I +W +A ++ P +\*\*\* V + H  
Sbjct 132 LVIALVALERHQLIINPTWKPSISQAYLIVIIVACVSLPLFLANSILENVPHKHNSKA 191  
Query 188 -HFMVDARNRSPYLYSCWEMPEKGMRVTTVLFISHIYLAPLALIVVMYARIARKLCQA 246  
\*+ D C EWP +V+YT L Y PL I+YARI R+L +  
Sbjct 192 LEFLADK-----VVCCTESPLAHRRHTTTFLLQPCYCLPGLFPLVCYARIRYRLRQ 244  
Query 247 PGPAPGGEAADPRASSRRAARVWHLWVMAVPLFTLWPLMALLLIDYQQLSAPOLHLV 306  
G + RA + +V++ +F + WLP+ +D+ +P H 306  
Sbjct 245 GRVPHRGTYSL--RAGHMK-QVNQVVLVMVAVFALWLPJLHJVFNLSLEDWHHEAIPICHQH 301  
Query 307 TYVIAFFPAHHLAFFNNSANPPIIYGYFNENFRFRGQ 342  
Sbjct 302 LI--FLVCHLLAMASTCVNPPIIYGFNLNTNFKEIKEA 335

>ref|NP\_001048.2| **G** tachykinin receptor 2 [Homo sapiens]  
dbj|BAC05952.1| **G** seven transmembrane helix receptor [Homo sapiens]  
Length=398

Gene ID: 6865 TACR2 | tachykinin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 145 bits (366), Expect = 3e-34, Method: Compositional matrix adjust.  
Identities = 117/408 (28%), Positives = 183/408 (44%), Gaps = 25/408 (6%)

Query 21 NTETATPATHTNFTSSYYQHTSPVAAAMPFIVAYALIPLLCMVGNHTLVCFLVJLQRNH 80  
N + P+N+T + + S + A+ + Y + L + C + V + I+V + R + M T VTH  
Sbjct 11 NISGPESENNTGIIATFASPMQSLQIALTAYLIVIAVIGNAIVIWLHRRHMRHTVNY 70  
Query 81 FILIAIAVSDDLWLGIFCMPTTLVONLITGMPFDNATCNCMGLVQGMGSVASVFTLVAIAVE 140  
F+I+A+ +DL + F V + W F A C L + + S+\*\*\* AIA +  
Sbjct 71 FVIALALADCMAAFAUNAFNPVYASHNNIYGRFACYFQNLPITAMPFSISIYMTAAAD 130  
Query 141 EPRCIVVHPFREKLRLKAVALTIAVIALALLIMCPNSVLTUTVREHEHHFMVDAARNRSPY 200  
R+ IVHPFP+ +I+ +A + AD + P TTV +  
Sbjct 131 RYMIAVVHPFPQRSLAPSTAKVACIYLWVLAVALASQPCYFSTVHDO-----GA 178  
Query 201 YSCNEAWPEKGMR-----VTTVLFISHIYLAPLAIJWVMMYARTARKLCQAGPAGPGEA- 256  
C AWP+ +Y + V+ +Y + IV PL+A + V Y+ I L + P G+A  
Sbjct 179 TKCVVAAWPDSGGKTLIYLWVLAVALITYLFLPLAVWMPVAVSIVGLTLMRRAVPP--GQAH 235  
Query 257 -ADPASRASRARVWHLWVMAVPLFTLWPLWALLLIDYQQLSAPOLHLVTVVYAPPFH 315  
A+ R + +V + +V V L F + WLP +L + + +V Y  
Sbjct 236 GANHLQAOQKFKVTKNLLVUUTPAFVWVLAVALASQPCYFSTVHDO-----GA 293  
Query 316 WLAFPNNSANPIIYGFVNLPNRGFOAARLARLCPRGSGSHKEAYSERPGQGLLHRFVV 375  
WIA + + NPPII+ +FV GP+ APR CP + + + P L RV  
Sbjct 294 WLAASSTWNMYPITTYCILHNRPSRFOARLARLCPRGSGSHKEAYSERPGQGLLHRFVV  
-WVSDWVTPPTTLELXELPLTTLSLSTRVNRC 351  
Query 374 VRPSDSDGLPSEEGPSGAPRGRGLLQSUERVHHLPEREGNGCSELPL 423  
Sbjct 352 HTKTELJPMGDTAPSEATSGEAGR-PQDSLWPGVGLLAPTKNTHWEI 398

>gb|AA07759.1| **G** pancreatic polypeptide receptor  
gb|AAV68196.1| **G** pancreatic polypeptide receptor 1 [Homo sapiens]  
gb|AAH6238.1| **G** Pancreatic polypeptide receptor 1 [Homo sapiens]  
Length=375

Gene ID: 5540 PPYR1 | pancreatic polypeptide receptor 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 145 bits (365), Expect = 3e-34, Method: Compositional matrix adjust.  
Identities = 103/336 (30%), Positives = 167/336 (49%), Gaps = 19/336 (5%)

Query 14 PLSQNGTNTTEATPATHTNFTSSYYQHTSPVAAAMPFIVAYALIPLLCMVGNHTLVCFLVJLQRNH 73  
P S G N T F PS + O V + \*++ + \*+\* ++ +GN + \*++ +  
Sbjct 12 PKSPOGENRSKPLGTYPNFNSCQSDVWDVNVFIVTYSIETVVGLVGLNLICMCTVTRQNE 71  
Query 74 MHTVTINMPFIANLAWSDLWLGIFCMPTTLVONLITGMPFDNATCNCMGLVQGMGSVASVFT 133  
VTN+ I NLA SD L+ C P T V + + M F CMKS +O MSV+ S+  
Sbjct 72 KANVNLJIANLAFAFSDFMLCQLQPIVATVYDYMWIGETLCKMSAFIQCSMSVTVSILS 131  
Query 134 LVIAIAVERFCIVHPFREKLRLKAVALTIAVIMALALLIMCP---SAVLTUTVREHE--- 187  
LV+A+ER+ +I+P+ K ++ +A + I +W +A ++ P +\*\*\* V + H  
Sbjct 132 LVIALVALERHQLIINPTWKPSISQAYLIVIIVACVSLPLFLANSILENVPHKHNSKA 191  
Query 188 -HFMVDARNRSPYLYSCWEMPEKGMRVTTVLFISHIYLAPLALIVVMYARIARKLCQA 246  
\*+ D C EWP +V+YT L Y PL I+YARI R+L +  
Sbjct 192 LEFLADK-----VVCCTESPLAHRRHTTTFLLQPCYCLPGLFPLVCYARIRYRLRQ 244  
Query 247 PGPAPGGEAADPRASSRRAARVWHLWVMAVPLFTLWPLMALLLIDYQQLSAPOLHLV 306  
G + RA + +V++ +F + WLP+ +D+ +P H 306  
Sbjct 245 GRVPHRGTYSL--RAGHMK-QVNQVVLVMVAVFALWLPJLHJVFNLSLEDWHHEAIPICHQH 301  
Query 307 TYVIAFFPAHHLAFFNNSANPPIIYGYFNENFRFRGQ 342  
Sbjct 302 LI--FLVCHLLAMASTCVNPPIIYGFNLNTNFKEIKEA 335

>emb|CAG46748.1| **G** PYR1 [Homo sapiens]  
Length=375



>dbj|BAD92474.1| G neuropeptide Y receptor Y1 variant [Homo sapiens]  
Length=262

Query 159 LVIATIWINALALLIMCPASVTLVCTREE-HHFMVDARNRSYPLSCWEANPEKGMRVRYT 217  
 Sbjct 164 YGIVAINVNLWAVASSLFLPIYQVNMTDFPNTVLDAYDKD--YVCFCDFQFSDSHRLSYT 220

Query 218 TVLFSHITYLAPLAIVVMYARIKLT 243  
 Sbjct 221 TLLWLQLYGPGLCPICIPYKRV-RKL 245

>gb|AAI22552.1| **G** tachykinin receptor 3 [Homo sapiens]  
 Length=465  
 GENE ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 125 bits (315), Expect = 2e-28, Method: Compositional matrix adjust.  
 Identities = 100/386 (25%), Positives = 172/386 (44%), Gaps = 35/386 (9%)

Query 24 ATPATNLTFSSYYQHTSPVAAAMPFIYALIFLCLNCVGNTLWCFLVILXRNHRHHTVTNNFIL 83  
 Sbjct 68 SQWANLT--NQFVQPSWRALMSLAYGVVAVLNGLNLIWVNIILAHKMRNRTVTNYFLV 125

Query 84 NLAVSDBLWVHMLVMAFPFTLNLWVNLALLIDYQSLAPQIHLWVTPVAPPFHNLAPPF 143  
 Sbjct 126 NLAPSDASMAAFNLTWVFIYALIISMEYFGANCYCRQNFPPI2AVFASISYNTIAVDRYM 185

Query 144 CIVPHFREKLTLRKAIVTAVIWAVALALLIMCPASVTLVCTREEHHFMVDARNRSYPLS- 202  
 Sbjct 186 AIIIDLKPKRLSLSTATKIVIGLSIWLAPLAPFCOLY-----SKTKVMPGRTL 232

Query 203 CMEAMPKGMR--VTTTFLPSHITYLAPLAIVVMYARIKLCQAGPAGPGEERAADPRA 261  
 Sbjct 233 CFVQNPBGPKQHPTFYHIIIVLVCPLFLIMGITYTTIVGILTWMGGIREGDTCDKYHEQLK 292

Query 262 SRRARVHVMLVMAFPFTLNLWVNLALLIDYQSLAPQIHLWVTPVAPPFHNLAPPF 321  
 Sbjct 293 AKR--KVVKRMIIIVVMTPAFLCMLWVPHIYVITAIYQQLNRWKYIQQVYLASF--WLMMS 348

Query 322 SSNPILYQYGNENPNFRGPQAFPARLCP-----RPGSGHKEAYSERPGGLH 369  
 Sbjct 349 TMNPYIIVYCCCLMKRPRAGKF--RNCCPFIKVSSYDELELKTTTRFHPNQRQSSMYTVRM 406

Query 370 RRVVFVVRPDSDGLPSESSGPGSSQPR 395  
 Sbjct 407 ESMTVPFDPNADTTSRSSKKRKRATPR 432

>gb|AAE21706.1| **G** neurokinin-3 receptor; NK-3 receptor [Homo sapiens]  
 Length=465  
 GENE ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 125 bits (314), Expect = 2e-28, Method: Compositional matrix adjust.  
 Identities = 100/386 (25%), Positives = 172/386 (44%), Gaps = 35/386 (9%)

Query 24 ATPATNLTFSSYYQHTSPVAAAMPFIYALIFLCLNCVGNTLWCFLVILXRNHRHHTVTNNFIL 83  
 Sbjct 68 SQWANLT--NQFVQPSWRALMSLAYGVVAVLNGLNLIWVNIILAHKMRNRTVTNYFLV 125

Query 84 NLAVSDBLWVHMLVMAFPFTLNLWVNLALLIDYQSLAPQIHLWVTPVAPPFHNLAPPF 143  
 Sbjct 126 NLAPSDASMAAFNLTWVFIYALIISMEYFGANCYCRQNFPPI2AVFASISYNTIAVDRYM 185

Query 144 CIVPHFREKLTLRKAIVTAVIWAVALALLIMCPASVTLVCTREEHHFMVDARNRSYPLS- 202  
 Sbjct 186 I+ P + I+L + S + I+L + R + V + P + -----SKTKVMPGRTL 232

Query 203 CMEAMPKGMR--VTTTFLPSHITYLAPLAIVVMYARIKLCQAGPAGPGEERAADPRA 261  
 Sbjct 233 CFVQNPBGPKQHPTFYHIIIVLVCPLFLIMGITYTTIVGILTWMGGIREGDTCDKYHEQLK 292

Query 262 SRRARVHVMLVMAFPFTLNLWVNLALLIDYQSLAPQIHLWVTPVAPPFHNLAPPF 321  
 Sbjct 293 AKR--KVVKRMIIIVVMTPAFLCMLWVPHIYVITAIYQQLNRWKYIQQVYLASF--WLMMS 348

Query 322 SSNPILYQYGNENPNFRGPQAFPARLCP-----RPGSGHKEAYSERPGGLH 369  
 Sbjct 349 TMNPYIIVYCCCLMKRPRAGKF--RNCCPFIKVSSYDELELKTTTRFHPNQRQSSMYTVRM 406

Query 370 RRVVFVVRPDSDGLPSESSGPGSSQPR 395  
 Sbjct 407 ESMTVPFDPNADTTSRSSKKRKRATPR 432

>emb|CAA646291.1| **G** neuromedin K receptor [Homo sapiens]  
 Length=465  
 GENE ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 125 bits (314), Expect = 3e-28, Method: Compositional matrix adjust.  
 Identities = 95/366 (25%), Positives = 164/366 (44%), Gaps = 33/366 (9%)

Query 4 AMVUVVALIFLCLNCVGNTLWCFLVILXRNHRHHTVTNNFILWVNLALLIDYQSLAPQIHLWVTPVAPPFHNLAPPF 103  
 Sbjct 86 ALNSWLAGVVVVAVLGNLNLWVNIILAHKMRNRTVTNYFLVNLAPSDASMAAFNLTWVFIY 145

Query 104 NLITPPDNATCKMSGLVQGMGSVSAVSPFLVAVINBQVYVWVPPHFRPNTTIRKALVTA 163  
 Sbjct 146 ALHSNEYYPGANNCYCRQNFPPI2AVFASISYNTIAVDRYMAIDPLKPKRLSATAKIVG 205

Query 164 VVIALALLIMCPASVTLVCTREEHHFMVDARNRSYPLSCWEANPEKGMRVRYT 221  
 Sbjct 206 SIMWLQLYGPGLCPICIPYKRV-RKL 252

Query 222 SHIYIYLAPLALIVVMYARIKLCQAGPAGPGEERAADPRASSRRARVVMGLWVNLAPPF 281

+Y PL ++ + Y + L P ++ + +R +VV Me+V + F +  
 Sbjct 253 ILVYCFPLLINGITTYIVGILWGGEPIDGTCDKYHEQLKAKR--KVKVMMIIVVMMTFAI 310  
 Query 282 SWLPMLAWLLIDYQOOLSAQPHLHVTVYAPPFFANWLAFFNSSANPIIYQYFNMENFRGFO 341  
 Sbjct 311 CMLPYHYPITAIYQQLNRMKYIQVYLYASP-WLMAMSSTMVNPIIYCLCNKRFRAGPK 368  
 Query 342 AAFAARLCP-----RPGSHKEAYSERPQLLHRRVFWVVPSDSLGPSESQ 389  
 Sbjct 369 RAF--R CP ++ + H S + + VV P+\* S  
 RAF--RWCPCFIKVSSYDDELELKTRFHPRNRQSSMVTVRMESMTVVFDPDNDAATTTRSSRK 426  
 Query 390 SSGAPR 395  
 Sbjct 427 KRATPR 432

>ref|NP\_001050.1| **G** tachykinin receptor 3 [Homo sapiens]  
 sp|P29371.1 **G** RecName: Full=Neuromedin-K receptor; Short=NKR; AltName: Full=Neurokinin  
 B receptor; AltName: Full=NKR-3 receptor; Short=NK-3R;  
 AltName: Full=tachykinin receptor 3  
 gb|AAA36386.1| **G** neurokinin-3 receptor  
 gb|AAE23926.1| **G** tachykinin receptor 3 [Homo sapiens]  
 gb|AAI21807.1| **G** Tachykinin receptor 3 [Homo sapiens]  
 gb|BAK06173.1| **G** tachykinin receptor 3 [Homo sapiens]  
 Length=465  
 Gene ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 125 bits (31c), Expect = 3e-28, Method: Compositional matrix adjust.  
 Identities = 95/366 (25%), Gaps = 164/366 (44%), Gaps = 33/366 (9%)  
 Query 44 AMIVAYALIPFLLCMVNTLICPVTLNQHNRHMHTVNNPFLNLAVASDILWIGCFCMPFTLV 103  
 Sbjct 86 AAMSLAYGVVVAQAVLGNLIVIWLHQNRTVINYPIVNLVLSDFASMAAFTNLVNFY 145  
 Query 104 NLITGMWPFNACTK9MSQVMSVSASVFTPLVAIAVERPRLCIVHPFREKLRLKALVLT 163  
 Sbjct 146 ALSEMYEYFGANCRQNPFFTTAVIATVAFSISMTAIAVCRYMIAIDPJKMPLRSATATKIVG 205  
 Query 164 VTIALALLINCMPSAVTLTVTREHHHPWDARNSVPLYS-CWEAMPKGMR-VITYTFLF 221  
 Sbjct 206 SIMIAlFLLAEPQCQLY-----SKTKVMPGRITLCPVQNPBPQHQHPTHYIIIVI 252  
 Query 222 SHIYLALIIVVWARIARKELCQAGPAGPGEAEADPRAVSARVWVHMLVWVALIFPTL 281  
 Sbjct 253 ILVYCFPLLINGITTYIVGILWGGEPIDGTCDKYHEQLKAKR--KVKVMMIIVVMMTFAI 310  
 Query 282 SWLPMLAWLLIDYQOOLSAQPHLHVTVYAPPFFANWLAFFNSSANPIIYQYFNMENFRGFO 341  
 Sbjct 311 CMLPYHYPITAIYQQLNRMKYIQVYLYASP-WLMAMSSTMVNPIIYCLCNKRFRAGPK 368  
 Query 342 AAFAARLCP-----RPGSHKEAYSERPQLLHRRVFWVVPSDSLGPSESQ 389  
 Sbjct 369 RAF--R CP ++ + H S + + VV P+\* S  
 RAF--RWCPCFIKVSSYDDELELKTRFHPRNRQSSMVTVRMESMTVVFDPDNDAATTTRSSRK 426  
 Query 390 SSGAPR 395  
 Sbjct 427 KRATPR 432

>gb|AAH05527.1| **G** TACR3 protein [Homo sapiens]  
 Length=464  
 Gene ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 124 bits (31l), Expect = 7e-28, Method: Compositional matrix adjust.  
 Identities = 100/386 (25%), 170/386 (44%), Gaps = 35/386 (%)  
 Query 24 ATPATNITPFSYYQNTSPVIAAMPVAYALIPFLLCMVNTLICPVTLNQHNRHMHTVNNPFL 83  
 Sbjct 67 SQWTWNTL-NQFQVPSRMRALPNSLAYQVAVAVLQLNLIVIWLHQNRTVINYPIVFL 124  
 Query 84 NHAVSHULWUJ1PMTTIVLN1U1YH1VYUNATCKAUSGLVQ3MSVSASVFTPLVAIAVERP 143  
 Sbjct 125 NLA SD + P + L + W F C +V AS+++++ATAVR+ 164  
 Query 144 C1VPHPREKLTIRKALVITAVIMALALLCPSVATLTVTREHHHPMDARNNSVPLYS- 202  
 Sbjct 185 AIIIDPLEPELSSTATATKIVGSIWILALFAPQCQLY-----SKTKVMPGRTL 231  
 Query 203 CWEAMPKGMR-VITYTFLVSHIYLALIIVVWARIARKELCQAGPAGPGEAEADPRA 261  
 Sbjct 233 CFVQNPBPQHQHPTHYIIIVLWVYLCPPFLIMIYTIVGIGLWGGEEIPGDTCDKYHEQLK 291  
 Query 262 SRRRAARVW6MLVWMLAWPLFTLSLWLPIWALLLIDYQOLSAQPHLHVTVYAPPFAHMFN 321  
 Sbjct 292 AKR--KVKVMMIIVVMMTFAICLWPHYHIVFLTIAIYQQLNRMKYIQVYLYASP-WLMAMS 347  
 Query 322 SSSNPPIIYQYVPMENFRGQPAQAFARLCP-----RPGSHKEAYSERPQLLH 369  
 Sbjct 348 TMWVPIIYCC1KNNRFRAGPKR--RWCPCFIKVSSYDDELELKTRFHPRNRQSSMVTVRM 405  
 Query 370 RRVYVWVPPSDSGLPSESEGSPSGAPR 395  
 Sbjct 406 ESMTWVFDPNDAATTTRSSRKKRATPR 431

>sp|Q13585.1|MTR1L\_HUMAN **G** RecName: Full=Melatonin-related receptor; AltName: Full=G protein-coupled receptor 50; AltName: Full=MT9  
 gb|AAC50614.1| **G** melatonin-related receptor  
 Length=613

GENE ID: 9248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]  
(Over 10 PubMed links)

Score = 123 bits (308), Expect = 1e-27, Method: Compositional matrix adjust.  
Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

Query 52 LIFLLC-----MVGNLTWCIVLKNRHMVTNTMFIILNLAVSDLVVGICMPPTLV 102  
+IP+ C +GN+V W KN+ +N+F+++L+V D+D+I+ P L  
Sbjct 28 IIPMFACAMVITIVDVLGNNGVILWATVTKKKLNNSGNIFFVVSLSVADMLVAIYPPMLMH 87

Query 103 DLNLITGPFPONATCGMSLGVMGSVASAVPFLVIAVERFRCIVHVPTREX -LTLRKALV 160  
I GM +C M G +S+V S+F +WIA+ R+ I H + + +R +  
Sbjct 88 AMSIGQWLSQLQCMQMGFTLQGVSISIWNIAVAINRNRYCYICHSLOYERIPSVRNTCI 147

Query 161 TIAVIVALALLIMCPASVTLTIVREHHHPMVDMARNRSYPLYSCEAMPEKOMBRVYTTLV 220  
+ W + I + P + T+ D R Y+C + V+T +  
Sbjct 148 YLVIWITWMTVLIAVLPNNYIOTG-----YDPRT-----YTCIPNYLNNP---VPTVTI 192

Query 221 FSHIYLAPLAIIIVVMARYARIKLQCAQPGAKGEEDAPRASRRARAVVHMLVWVALFFT 280  
+ PL + L+L+ +S ++ + + + A++A+PNS N +IYG NENFR  
Sbjct 193 VCINHPVLPILLIUVGFCYRINTVKVLAARDPA----GQNPDNOLAEVRNFLTMVFLGFA 247

Query 281 LSWLPLWALLLLIDYQQLSAPQH-LTVTYAAPPFHAWLFNFNSSAMPIIYGYPNENFRG 339  
+ W P+ L+L+ +S ++ + + + A++A+PNS N +IYG NENFR  
Sbjct 248 VCPCPINVLTVLV--AVSPKEMAGKIPNWLILYAAYFIAYFNSCLNAVIYGLNNENFR 304

Query 340 FQAFRA 346  
Sbjct 305 YNTIFHA 311

>ref|NP\_004215.2| **G** G protein-coupled receptor 50 [Homo sapiens]  
Length=617

GENE ID: 9248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]  
(Over 10 PubMed links)

Score = 123 bits (308), Expect = 1e-27, Method: Compositional matrix adjust.  
Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

Query 52 LIFLLC-----MVGNLTWCIVLKNRHMVTNTMFIILNLAVSDLVVGICMPPTLV 102  
+IP+ C +GN+V W KN+ +N+F+++L+V D+D+I+ P L  
Sbjct 28 IIPMFACAMVITIVDVLGNNGVILWATVTKKKLNNSGNIFFVVSLSVADMLVAIYPPMLMH 87

Query 103 DLNLITGPONATCGMSLGVMGSVASAVPFLVIAVERFRCIVHVPTREX -LTLRKALV 160  
I GM +C M G +S+V S+F +WIA+ R+ I H + + +R +  
Sbjct 88 AMSIGQWLSQLQCMQMGFTLQGVSISIWNIAVAINRNRYCYICHSLOYERIPSVRNTCI 147

Query 161 TIAVIVALALLIMCPASVTLTIVREHHHPMVDMARNRSYPLYSCEAMPEKOMBRVYTTLV 220  
+ W + I + P + T+ D R Y+C + V+T +  
Sbjct 148 YLVIWITWMTVLIAVLPNNYIOTG-----YDPRT-----YTCIPNYLNNP---VPTVTI 192

Query 221 FSHIYLAPLAIIIVVMARYARIKLQCAQPGAKGEEDAPRASRRARAVVHMLVWVALFFT 280  
+ PL + L+L+ +S ++ + + + A++A+PNS N +IYG NENFR  
Sbjct 193 VCINHPVLPILLIUVGFCYRINTVKVLAARDPA----GQNPDNOLAEVRNFLTMVFLGFA 247

Query 281 LSWLPLWALLLLIDYQQLSAPQH-LTVTYAAPPFHAWLFNFNSSAMPIIYGYPNENFRG 339  
+ W P+ L+L+ +S ++ + + + A++A+PNS N +IYG NENFR  
Sbjct 248 VCPCPINVLTVLV--AVSPKEMAGKIPNWLILYAAYFIAYFNSCLNAVIYGLNNENFR 304

Query 340 FQAFRA 346  
Sbjct 305 YNTIFHA 311

>gb|AAI03697.1| **C** GPR50 protein [Homo sapiens]

gb|AAI05684.1| **G** GPR50 protein [Homo sapiens]  
Length=617

GENE ID: 9248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]  
(Over 10 PubMed links)

Score = 122 bits (307), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

Query 52 LIFLLC-----MVGNLTWCIVLKNRHMVTNTMFIILNLAVSDLVVGICMPPTLV 102  
+IP+ C +GN+V W KN+ +N+F+++L+V D+D+I+ P L  
Sbjct 28 IIPMFACAMVITIVDVLGNNGVILWATVTKKKLNNSGNIFFVVSLSVADMLVAIYPPMLMH 87

Query 103 DLNLITGPONATCGMSLGVMGSVASAVPFLVIAVERFRCIVHVPTREX -LTLRKALV 160  
I GM +C M G +S+V S+F +WIA+ R+ I H + + +R +  
Sbjct 88 AMSIGQWLSQLQCMQMGFTLQGVSISIWNIAVAINRNRYCYICHSLOYERIPSVRNTCI 147

Query 161 TIAVIVALALLIMCPASVTLTIVREHHHPMVDMARNRSYPLYSCEAMPEKOMBRVYTTLV 220  
+ W + I + P + T+ D R Y+C + V+T +  
Sbjct 148 YLVIWITWMTVLIAVLPNNYIOTG-----YDPRT-----YTCIPNYLNNP---VPTVTI 192

Query 221 FSHIYLAPLAIIIVVMARYARIKLQCAQPGAKGEEDAPRASRRARAVVHMLVWVALFFT 280  
+ PL + L+L+ +S ++ + + + A++A+PNS N +IYG NENFR  
Sbjct 193 VCINHPVLPILLIUVGFCYRINTVKVLAARDPA----GQNPDNOLAEVRNFLTMVFLGFA 247

Query 281 LSWLPLWALLLLIDYQQLSAPQH-LTVTYAAPPFHAWLFNFNSSAMPIIYGYPNENFRG 339  
+ W P+ L+L+ +S ++ + + + A++A+PNS N +IYG NENFR  
Sbjct 248 VCPCPINVLTVLV--AVSPKEMAGKIPNWLILYAAYFIAYFNSCLNAVIYGLNNENFR 304

Query 340 FQAFRA 346  
Sbjct 305 YNTIFHA 311

>gb|AAI05685.1| **G** G protein-coupled receptor 50 [Homo sapiens]

gb|ABY87917.1| **G** G protein-coupled receptor 50 [Homo sapiens]  
Length=613

GENE ID: 9248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]  
(Over 10 PubMed links)

Score = 122 bits (307), Expect = 2e-27, Method: Compositional matrix adjust  
Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

Query	52	L1FLLC-----MVGNTLWCFV1VLRQHRRMTTBTMQLN-ASVLSLW1FCHPMLTLV +IPC-----+GN+-----Y KM+-----N+F+-----D+L+D+V+L+ Sbjct 28 I1IPCMAMVIT1VLDLNGNSV1LWLTVKNCKLLENSG1FVPSLSVADMILVAIY1PPMLMH	102
Query	103	DNL1TRPFDATNCMGLVQSGNSAUSVFLVIAJAVERFCV1FPPRFER---LTLRKA C+H 1 G+-----+G+S +-----S+P+-----V+-----+R+ Sbjct 88 AMSIGGMDDLSQLSQLQCMYGPFTLGSV1S1P1VATAN1TNYC1C1CSLQYERFISVNTC1	147
Query	161	TIAVIALAWAL-----MSVPAVLTVTFVREHHWMDARNRSLVY1SCWAMPEKKGRRVTTVL Sbjct 148 YLVITNIMTIVLAVLNMYGTTIE-----YDPRT-----YTC1FNLHNJP-----VFTV1	224
Query	221	FSHY1LAFLP1LLVMYAR1TAKLQCAQPGPFGEEADPRASRERARVWHMMLWMPFT ++ PL +-----C+H A PA +-----+ +-----+ L F Sbjct 193 VCH1FVPL1V7GCFV1R1TKVLA1W1-----GQNPDNFQLAERVNTPMFV1PTW1	247
Query	281	L5WL1N1W1L1L1D1GQ1S1Q1G1-----LWT1VAFPFARH1LFPPNS1I1CYG1NENFR1 Sbjct 248 S+L+ +-----S+*** + + +-----A+***+ PNS + N + YG1NENFR1 VCNP1N1V1T1V1-----AVSPKNA1GK1N1L1L1L1A1Y1TNS1C1A1V1Y1N1R1	339
Query	340	FAQFAFR1 346	304
Sbjct	305	Y1T1F1 311	

>gb|EAW99402.1| G G protein-coupled receptor 50 [Homo sapiens]  
Length: 612

GENE ID: 9248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]

Score = 122 bits (307), Expect = 2e-27, Method: Compositional matrix adjust  
Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

```
>ref[NP_001718.1] UG bombesin-like receptor 3 [Homo sapiens]
|sp|P32247.1|BR3 HUMAN G RecName: Full=Bombesin receptor subtype-3; Short=BRS-3
|gb|AAA5604.1| G bombesin receptor subtype-3
|emb|CAA54031.1| G uterine bombesin receptor [Homo sapiens]
|emb|CAB10731.1| G bombesin-like receptor 3 [Homo sapiens]
|gb|AT774946.1| G bombesin-like receptor 3 [Homo sapiens]
|gb|EAWB470.1| G bombesin-like receptor 3 [Homo sapiens]
```

GENE ID: 680 BRS3 | bombesin-like receptor 3 [Homo sapiens]  
(Over 10 PubMed links)

<http://www.usenix.org/events/bsdi/bsdi99/>









```

>ref[NP_001044.1] LG somatostatin receptor 5 (Homo sapiens)
sp|P35346.1|SSRS_HUMAN C RecName: Full=Somatostatin receptor type 5; AltName: Full=SST5;
dbj|ABA04107.1| C fifth somatostatin receptor subtype [Homo sapiens]
gb|[ABAB31829.1| C somatostatin receptor subtype SSTR5, SRIF receptor subtype SSTR5
[human, Peptide, 364 aa]
gb|[ALAB8744.1| C somatostatin receptor subtype 5 [Homo sapiens]
gb|[RAN85687.1| C somatostatin receptor 5 [Homo sapiens]
Length=364

GRIN ID: 6755 SSTR5 | somatostatin receptor 5 [Homo sapiens]
(Over 10 PubMed links)

Score = 117 bits (239), Expect = 9e-26, Method= Compositional matrix adjust.
Identities = 94/312 (30%), Positives = 148/312 (47%), Gaps = 40/312 (12%)

Query 60 GHITKCFIQLVNRKQVWVFLMILFVNLVSDLWVGIVFCMTCVLLDVLHILQHDFNDATCKMS 119
Sbjct 57 GNTLYIYVWLRPAKMRKTTVLLVLAQDVLY-MLGFLPLATONASQFPWGPVVLRLV 119

Query 120 GLYVNOVSASVTFVAVIAVTFRCVYVHPFKRTEKLTLAHLVTT--NIVNLALLIMGOSA 177
Sbjct 61 G+-----SVP L-----V-----P-----R-----A-----M-----P----- 177
Sbjct 116 MLDLVDNQPTSFVFLC7VMSVDRYLAVHPLSSARWRPRVPLAASAAVMLSLCLMPL 175

Query 178 VTLVLTREHHFVMDARNSRTSYLCSKEMPE----KSHRRVVTYVLLVPLAHLALI 232
Sbjct 176 V-----C+-----+-----+-----+-----+-----+-----+-----+----- 232
Sbjct 176 VFADVQCGGG ----TCNASASPEFWGLWGAIVPIIYTVLQG----FPFLAVLI 217

```

Query 233 VVYARIAKELCQAPGPGEEAADPRASRERVRVHMLWVALPFTLSPMLPLWALLLLI 292  
**Sbjct** 218 CCLCYLIVVKV---RAVGRVGCCRRSRR---KVTMVLVLLVLFQGKLPPTFVNIV 270

Query 293 IDYGQALAPOLHVVTFVAPPNMLAHPFNNSANPIIYGYVNFENPFRGFQAAFRALCRCP 352  
**Sbjct** 271 --NLAVALPQ--EPASAGLYFFVVIYLISYANSANCVPVLYGFLPSDNDRFSQPKV---LCIRK 323

Query 353 SGSHKRAYSER 364  
**Sbjct** 324 GSGAKDADTTEP 335

>ref|NP\_004239.1| **[G]** G protein-coupled receptor 10 [Homo sapiens]  
 gb|P46831.2| PRHLR HUMAN **[G]** RecName: Full=Prolactin-releasing peptide receptor; Short=PrRPR; AltName: Full=G-protein coupled receptor 10; Short=HGR3  
 dbj|[BA3A1155.1] **[G]** human prolactin-releasing peptide receptor [Homo sapiens]  
 8 more sequence titles

dbj|[BAB83030.1] **[G]** prolactin releasing peptide receptor [Homo sapiens]  
 gb|AAH95539.1| **[G]** PRLHR protein [Homo sapiens]  
 gb|AAI01491.1| **[G]** PRLHR protein [Homo sapiens]  
 gb|AAI01493.1| **[G]** PRLHR protein [Homo sapiens]  
 gb|EAM49413.1| **[G]** prolactin releasing hormone receptor, isoform CRA\_a [Homo sapiens]  
 gb|EAM49414.1| **[G]** prolactin releasing hormone receptor, isoform CRA\_a [Homo sapiens]  
 gb|ABG52422.1| **[G]** prolactin releasing hormone receptor [Homo sapiens]  
 dbj|[BAE83150.1] **[G]** unnamed protein product [Homo sapiens]  
 Length=370

Gene ID: 2834 PRLHR | prolactin releasing hormone receptor [Homo sapiens]  
 (Over 10 PubMed links)

Score = 117 bits (292), Expect = 9e-26, Method: Compositional matrix adjust.  
 Identities = 100/305 (32%), Positives = 152/305 (49%), Gaps = 25/305 (8%)

Query 60 GNTLFCVIFVLLNRHNRHNTTNPMLLAVSDELLWGLFMPPTLWDNLN-TGMPDNATCNS 118  
**Sbjct** 67 GNLCLVLLVIAARVNPMLLAVSDELLWGLFMPPTLWDNLN-TGMPDNATCNS 136

Query 119 SGLVQGMGSVASVTFVVAIPTERPRCIVHPPREKLTIRLAQVIAVITNALVALLNCMPASV 178  
**Sbjct** 137 VPFLLPMTVYVSVTFVLTIAVQYVWVLLVPHLRKKISLRLSISYANVAVLATMLAVALPAV 196

Query 179 TLTVTREIEHHPMVDAWRNSPLYSQCMWEA 237  
**Sbjct** 197 H + V + + L C E W + R + Y + L YL PL I+ +  
 ---HHTWLEPKRPLW---CSEPPQGQERORQJQYANGLILVTTPLDNLVITLISVY 246

Query 238 RIKRALKQACPGPQGEGEADPRASRERARVHMLWVALPFTLSPMLPLWALLLLI 297  
**Sbjct** 247 RVSVLKLNRNVPGCVCQSADMDRARRKKTPTC-LDVVVVVVFAVCHLQWLVNLLRQDQP 305

Query 298 LSPAHUHLLTVYAAP----FARHMLAFTNSANPIIYGVNFENPFRGFQAAFRALCRPS 353  
**Sbjct** 306 ---HAIDPYAPEGVQLQHCLWLMSAACSYNPPIYAWLHSDSFREELRKLUVW---PRKI 357

Query 354 GSBBKE 358  
**Sbjct** 358 APHQO 362

>gb|AAF42810.1|**[A]** AFI81474\_2 **[G]** somatostatin receptor 2B [Homo sapiens]  
 gb|EAM89111.1| **[G]** somatostatin receptor 2, isoform CRA\_a [Homo sapiens]  
 Length=356

Gene ID: 6752 SSTR2 | somatostatin receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 116 bits (291), Expect = 1e-25, Method: Compositional matrix adjust.  
 Identities = 97/356 (27%), Positives = 163/353 (46%), Gaps = 43/353 (12%)

Query 1 MEGSCQPPNS---SMPSQGKQVTPAIPFVAFVPAHNFSSYQHTSPVAVMPLWALIYLICLM 58  
**Sbjct** 3 MEGSCQPPNS---SMPSQGKQVTPAIPFVAFVPAHNFSSYQHTSPVAVMPLWALIYLICLM- 59

Query 59 VGNLTCFVCFVLLNRHNRHNTTNPMLLAVSDELLWGLFMPPTLWDNLN-TGMPDNATCNS 118  
**Sbjct** 60 GNTLTCFVCFVLLNRHNRHNTTNPMLLAVSDELLWGLFMPPTLWDNLN-TGMPDNATCNS 117

Query 119 SGLVQGMGSVASVTFVVAIPTERPRCIVHPPREKLTIRLAQVIAVITNALVALLNCMP 175  
**Sbjct** 118 VMTVDGQINOPTSFCVLTNSISDLYWVLPVPIKSAWNSRPRPXTAMITMVAM-WGVSLLVILP 176

Query 177 SATVLTIVTREIEHHPMVDAWRNSPLYSQCMWEA 233  
**Sbjct** 177 IMI-----YAGLSLNQWQGESSCTTNIWIGESGAWYGPPIYTFILGFLPLWPLTTC 225

Query 234 VVYARIAKELCQAPGPGPEERAADPRASRERVRVHMLWVALPFTLSPMLPLWALLLLI 293  
**Sbjct** 226 CCLCYLIIKV---EKGSSQPKHCKSEKVKTTMWSVSIWVAVPFCMPPY---IF 275

Query 294 DYGQLS---APOLHVVTFVAPPNMLAHPFNNSANPIIYGYVNFENPFRGFQ 341  
 + S P L + F L + NS AMP1+ + ++NPF+ PQ

Query 272 NVSSVMSAISPTPALPKGM---FDPVVVLITYANSANCAMPVLYAFLSPDFKPSQK 324

>ref|NP\_658986.1| **LG** prokineticin receptor 2 (Homo sapiens)  
sp|Q8NWJ6.1|PKR2 HUMAN **C** RecName: Full=Prokineticin receptor 2; Short=PK-R2; AltName:  
Full=G-protein coupled receptor 73-like 1; AltName: Full=GPR73b;



Query 294 DYQQLS----APQHLHLVTVYAFFWLAFFNNSANPPIIYGFNFENFRRGFOQA-P-RAR 347  
 Sbjct 276 \* +S P L + F F L + N S ANPPI+Y + ++NF++ FO +  
 MVSSVSMASIPSPALKGM--PFDVVVLLTIANSCAMPILYAFLSONFKRSFQNVLCLVK 331  
 Query 348 LCPRPGSGSHKEAYSER 363  
 Sbjct 332 VSGTDDGERSDSKQDK 347

>gb|AAH95542.1| **G** Neuromedin B receptor [Homo sapiens]  
 Length=390  
 GENB ID: 4829 NMNR | neuromedin B receptor [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 115 bits (289), Expect = 2e-25, Method: Compositional matrix adjust.  
 Identities = 89/320 (27%), Positives = 152/320 (47%), Gaps = 26/320 (8%)  
 Query 50 YALIFLCLCNGNTLVCFLVIVLNRRHHTVTNNFLNLLAVSLDLVGLICMPTTLVDNLITGW 109  
 Sbjct 50 YLLITVVLGNNIMWLKVFPTTSMSRVSNPVNPISNLAJGDLILLTCVFDASRYFPDEW 109  
 Query 110 PPDNATCKMGSLVQGMSVSASVFTLVAAIWERFRCVWHPPREKL-T-LRKALVTTIAVIMA 167  
 Sbjct 110 P CK+ ++Q M +V N +F1 NLA DLL+ +C+P + + + +F +  
 MPGVVGCKLIPV1QLTSTVGSVFTTIALSADRYRAVINPNMDQTSQALLRTCVANGIMV 169  
 Query 168 LALLIMCPASVTLVTREEHHHFDWARRHHTVYAFFSYPLYSCEAMPEKGR--RVTYTTVLFSHIY 225  
 Sbjct 170 VSVLJAVPEPVPSKVAR--+ISLSDNNSPT--ACI-PYPCOTDELPK1HSVLiPLVYF 221  
 Query 226 LALLIMCPASVTLVTREEHHHFDWARRHHTVYAFFSYPLYSCEAMPEKGR--RVTYTTVLFSHIY 285  
 Sbjct 222 LALLIMCPASVTLVTREEHHHFDWARRHHTVYAFFSYPLYSCEAMPEKGR--RVTYTTVLFSHIY 281  
 Query 286 LALLIMCPASVTLVTREEHHHFDWARRHHTVYAFFSYPLYSCEAMPEKGR--RVTYTTVLFSHIY 343  
 Sbjct 282 NHILYMMRSRPNYNEIOPSLGHMIVLTVL--ARVLsFGNSCNVPFALYLLSESRRHPN-- 336  
 Query 344 FRALICPSPSGSHKEAYSER 363  
 Sbjct 337 -+L C ---++Y ER 349

>gb|ABQ52418.1| **G** prokineticin receptor 2 [Homo sapiens]  
 Length=384  
 GENB ID: 128674 PROKR2 | prokineticin receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 115 bits (289), Expect = 2e-25, Method: Compositional matrix adjust.  
 Identities = 86/373 (23%), Positives = 173/373 (46%), Gaps = 41/373 (10%)  
 Query 16 SONGNTITEATP--ATNLTPS-SYONTSPV-- -RAMPIVAYAL- 52  
 Sbjct 16 +ONG NT TP - A+LcP+ SY + \* AA ++ AL 61  
 AQQ-NTSPTRNFNPQDQHNFQGYDOLPM+DEDEDMTKTTRPFKAIVIGIALA 61  
 Query 53 -ITLLOMGNLTLVCFIVLQRNBMGTJTHNFWLAVSLDLWGLICMPTTLVDNLITGW 109  
 Sbjct 53 I,Lc +Q+ + + + + +TN+ I NLA-SD LV I C P + ++ N 121  
 GIMLWCGIGNFVFAAIIYTRVKKLRLNTHLJIANLAISDFLVAIACCCPFEHDYVQRLQSLN 121  
 Query 110 PPDNATCKMGSLVQGMSVSASVFTLVAAIWERFRCVWHPPREKL-T-LRKALVTTIAVIMA 169  
 Sbjct 110 + C ++ S LAIA+R+ IVHP ++ + + A IA+H ++ EHGHLVLCASVNYLRTVSLVYSTNALLAIADYLAIVHLKPERFMNYQTAFSLIALVMVMS 181  
 Query 170 LLIMCPASVTLVTREEHHHFDWARRHHTVYAFFSYPLYSCEAMPEKGR--RVTYTTVLFSHIY 227  
 Sbjct 170 +L PSA T E B P + ++ C +W P ++ + Y +F ++ ILIAIAPSAYFAT--ETVLVFIKSQSKF---CGQINPFDQQLYK5YPLFPGVEFV 234  
 Query 228 PLALIYMMYARAKLCOAQPAGPGEAEADPRASERARRVHMLWVALWPLFTLSWLPW 287  
 Sbjct 228 Ps + + YARI+P R E+ RR +V M ++ A + L W P + PVMTMLCYLARSLWMPKAVPGPQTQEIKRGLKCRRTVILVIMCLITA--YVLCNAPFY 292  
 Query 288 ALLLIDYG-QSAPOLHLYTVYAPPARHPLAPPNSANDIYGFNFENFRRGFOA+PRA 346  
 Sbjct 293 GPTIVRDPFPTVVKERHYL--APYVCECIAMNSMINTMCPTVTKNNTMYKYFKKOML 350  
 Query 347 RLCPRPGSGSHKEAKA 359  
 Sbjct 351 HWRPSQRGSKSSA 363

>ref|NP\_002502.2| **G** neuromedin B receptor [Homo sapiens]  
 sp|P28336.2| **hMER\_HUMAN** **G** RecName: Full=Neuromedin-B receptor; Short=NMB-R; AltName: Full=Neuromedin-B preferring  
 homobolin receptor  
 emb|CAM70473.1| **G** neuromedin B receptor [Homo sapiens]  
 gb|EAH74866.1| **G** neuromedin B receptor [Homo sapiens]  
 Length=390  
 GENB ID: 4829 NMNR | neuromedin B receptor [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 115 bits (288), Expect = 3e-25, Method: Compositional matrix adjust.  
 Identities = 89/320 (27%), Positives = 152/320 (47%), Gaps = 26/320 (8%)  
 Query 50 YALIFLCLCNGNTLVCFLVIVLNRRHHTVTNNFLNLLAVSLDLVGLICMPTTLVDNLITGW 109  
 Sbjct 50 YLLITVVLGNNIMWLKVFPTTSMSRVSNPVNPISNLAJGDLILLTCVFDASRYFPDEW 109  
 Query 110 PPDNATCKMGSLVQGMSVSASVFTLVAAIWERFRCVWHPPREKL-T-LRKALVTTIAVIMA 167  
 Sbjct 110 P CK+ ++Q M +V N +F1 NLA DLL+ +C+P + + + +F +  
 MPGVVGCKLIPV1QLTSTVGSVFTTIALSADRYRAVINPNMDQTSQALLRTCVANGIMV 169  
 Query 168 LALLIMCPASVTLVTREEHHHFDWARRHHTVYAFFSYPLYSCEAMPEKGR--RVTYTTVLFSHIY 225  
 Sbjct 170 ++L P A V R V + N S + +C +P + + + +F +  
 VSVLJAVPEAVPSEVAR--+ISLSDNNSPT--ACI-PYPCOTDELPK1HSVLiPLVYF 221

Query 226 LAPALIVVYARIARKLCQAPGPAGPGEAAADPRASRRARVHMLVMVALFPTLSWLW 285  
 L PLA-I + Y IA+ L ++ PG + R R+ +++ F W P  
 Sbjct 222 LIPLAIIISIYVHYIAKTLKISAHNLPGYEYNEHTKKQMSTRKKLAKIVLTVFVGCFPCWP 281

Query 286 LWALLLL - IDYGOLSAQPHLHVTVYAPPFAHMLAFFFNSANPPIIYGYFVNENFRRGPFQAA 343  
 L + Y++ H+ A L-F NS NP +E+FRR F  
 Sbjct 282 NHILLYMRSFNVNEYIDPSLGHMIVTTLV--ARVLSGFGNCVNPFFALYLLSESFRRHFN- 336

Query 344 FRARLCPRPSSGSHKEAYSER 363  
 Sbjct 337 --SOLC----CGRKSYQSER 349

>gb|AAAS59939.1| **G** neuromedin B receptor  
 gb|AAAB27330.1| **G** neuromedin B receptor, NMB receptor=bombesin-like peptide receptor  
 [human, SCLC cell line H345, Peptide, 390 aa]  
 Length=390

GENE ID: 4828 NRBR | neuromedin B receptor [Homo sapiens]  
 (Over 10 PubMed links)

Score = 115 bits (288), Expect = 3e-25, Method: Compositional matrix adjust.  
 Identities = 85/320 (27%), Positives = 152/320 (47%), Gaps = 26/320 (8%)

Query 50 YALIFLCLCNVGHNTLFCFIVL1NRRHMHHTVNMFLNLAWSDLWLGIFCMTTLVDNLITGW 109  
 Y L+ +GN ++ M T +NLA+ D L + +P + W  
 Sbjct 50 YLITITVGLLNLIMDVKIPITNSAMSRRVNP1F1NSAAGDL+L+TCVPDASRYRPFDEW 109

Query 110 PFDNATCNGSGLWQMSVSASVPTLVIAAVERFRCIVHPPFREKL-T-LRKALVTTIAVIMA 167  
 CK+ +O SV STVFL A++ +R R VWP + L + V +W  
 Sbjct 110 MFGKVGCKLIPV1QLTSVGSVGTITLALSADRYRAVAVNPMDDMQTSQALRTCYKANGIRV 169

Query 168 LALLIMCPSAVLTIVTREHHFPMWDNRNSRSPLYSCWNEAMPEKEMR - RVVTTVLFSLHY 225  
 +-+L+ +PV V R + +S+ +S+ +P + W P  
 Sbjct 170 VSVLVLAVPEPVSEVAR-----ISSLDNSOPT---ACI-PYPQTDELHPKHNSVLLFLVNY 221

Query 226 LALIIVVNAKLRKLCQAPGPAGPGEAAADPRASRRARVHMLVMVALFPTLSWLW 285  
 PLA-I + Y IA+ L ++ PG + R R+ +++ F W P  
 Sbjct 222 LIPLAIIISIYVHYIAKTLKISAHNLPGYEYNEHTKKQMSTRKKLAKIVLTVFVGCFPCWP 281

Query 286 LWALLLL - IDYGOLSAQPHLHVTVYAPPFAHMLAFFFNSANPPIIYGYFVNENFRRGPFQAA 343  
 L + Y++ H+ A L-F NS NP +E+FRR F  
 Sbjct 282 NHILLYMRSFNVNEYIDPSLGHMIVTTLV--ARVLSGFGNCVNPFFALYLLSESFRRHFN- 336

Query 344 FRARLCPRPSSGSHKEAYSER 363  
 Sbjct 337 --SOLC----CGRKSYQSER 349

>gb|AAA36623.1| **G** somatostatin receptor  
 db|BA04106.1| **G** fourth somatostatin receptor subtype [Homo sapiens]  
 gb|AASS5549.1| **G** somatostatin receptor 4 [Homo sapiens]  
 gb|AAH69063.1| **G** Somatostatin receptor 4 [Homo sapiens]  
 gb|AAI17273.1| **G** Somatostatin receptor 4 [Homo sapiens]  
 Length=388

GENE ID: 6754 SSTR4 | somatostatin receptor 4 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 115 bits (287), Expect = 4e-25, Method: Compositional matrix adjust.  
 Identities = 92/308 (30%), Positives = 150/306 (49%), Gaps = 34/306 (11%)

Query 50 YALIFLCLCNVGHNTLFCFIVL1NRRHMHHTVNMFLNLAWSDLWLGIFCMTTLVDNLITGW 109  
 Y AL+ +VGN F+L+ M T M+ +LNLA+D L + +P + W  
 Sbjct 54 YALCVLCLGLVGNALVIFVYLARYAKTMATIYLNLAVALADELP-MLSVPFVASSAALRHL 112

Query 110 PFDNATCNGSGLWQMSVSASVPTLVIAAVERFRCIVHPPFREKL-T-LRKALVTTIAV-IMA 167  
 PP+ C+ V G+++ SVL P+ +V+R+ -VHP R R + + +W  
 PGSVLCRALVSVGDGLNMPSTSFCFLTVLSVDRYRAVAVHPLRAATYRRPSVAKLNLIGVML 172

Query 168 LALLIMCPSAVLTIVTREHHFPMWDNRNSRSPLYSCWNEAMPEKMRVVTTLVPSHYIL 226  
 +-+L+ P A+ D R +C W E V+ P +L+  
 Sbjct 173 ASLTLPLPIAI-----PARQDQQAQVACLQWPHFANSASVFPVYTFLLQFL 221

Query 227 APALALIVVYARIARKLCQAPGPAGPGEAAADPRASRRARVHMLVMVALFPTLSWLW 284  
 P+ I + Y I K+ A G++ RRR+ ++ +W+ F L W+  
 Sbjct 222 LPVLAIGLICLYLIVGKHM-RAVALRAGHQQ-----RRSEKXKTRLIVLWVVVFVLCWM 273

Query 285 PWLALLLL - IDYGOLSAQPHLHVTVYAPPFAHMLAFFFNSANPPIIYGYFVNENFRRGPFQAA 343  
 P + LL + L A H+ + L+- NS ANPI+Y+ +NFRR FQ  
 Sbjct 274 PFYVVLQNLNLVTVTSIDATVNHVSLI-----LSTANSCAMPILYGFPLSDMFRRSPQRV 325

Query 344 FRARL 349  
 R C  
 Sbjct 326 LCLRC 331

>gb|AAK12166.1| **G** somatostatin receptor type 5 [Homo sapiens]  
 Length=364

GENE ID: 6755 SSTR5 | somatostatin receptor 5 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 115 bits (287), Expect = 4e-25, Method: Compositional matrix adjust.  
 Identities = 93/307 (30%), Positives = 146/307 (47%), Gaps = 46/307 (13%)

Query 60 GNTLVCFLV1NRRHMHHTVNMFLNLAWSDLWLGIFCMTTLVDNLITGMPDNATCNGS 119  
 GNTLV+ +VL+ M TTVN+ +TFLNLA+D+V+ + W +NPW+C+  
 Sbjct 57 GNTLV+ +V+L+ M TTVN+ +TFLNLA+D+V+ + W +NPW+C+  
 LPVLAIGLICLYLIVGKHM-RAVALRAGHQQ-----RRSEKXKTRLIVLWVVVFVLCWM 115

Query 120 GLVQMSVSASVPTLVIAAVERFRCIVHPPFREKL-T-LRKALVTTI-AVINALIMCPSA 177  
 + G+ SVF L +V+R+ -VHP R + A W L+  
 Sbjct 116 MTQDQNPQTSVFCFLTVGSVDRYLA7VPLSARNRRPVRVAKLQSAMVYLSLQMSLPL 175

```

>ref|NP_005095.1| MTNR1B melatonin receptor 1B [Homo sapiens]
sp|P49286.1|MTNR1B Human RecName: Full-Melatonin receptor type 1B; AltName: Full-Mel
melatonin receptor; Short-Mel-1B-R
gb|[AAC05612.1| C Mel-1B-melatonin receptor
dbj|AAU2315.1| C melatonin 1b receptor [Homo sapiens]
gb|[AN00461.1| C melatonin receptor 1B [Homo sapiens]
gb|[AHS9163.1| C Melatonin receptor 1B [Homo sapiens]
gb|[EAW6891.1| C melatonin receptor 1B [Homo sapiens]
Length:362

GENE ID: 4544 MTNR1B | melatonin receptor 1B [Homo sapiens]
(Over 10 PubMed links)

Score = 114 bits (285), Expect = 6e-25, Method: Compositional matrix adjust.
Identities = 94/313 (31%) vs 143/313 (45%), Gap = 34/313 (10%)
Query 58 MVGRLWCPVTLKQNRHMVTNFMLILNLAVIDSLDGLVFCIMPTFLVDNLITGWPFDNATCK 117
+VGR LV WI+NR : N+F++I+A+D+L+ + P LV GH CK
Sbjct 55 VVGHLLVLSLRNLRRNLNAGNLFVLSIALADLVAPPYPPPLILVAFYDNGLAEHHCK 114

Query 118 MSGVLQGWSASAVPTVVAIAVEPRCIVHPPFRKLTLRK - ALTVIAALMALLICUMP 175
S  G+S V+ S+V+ A+T+ R- I H +R+ + I+V L+ ++ P+
Sbjct 115 ASAFAVQGSLVGSVPAITAIANRYCICHSMAYRHYTRRFLVLLWCLWLWITVALLP 174

Query 176 SAVTLTVTREHHWMDPDKRNLYPSLCSHEARPEKGMRHRVTVTLFHSIHLAPALILVV 235
Sbjct 175 -----+FP V+ +VSC + + + V- H + L+ PR+A+ +NPFPGSLEYLDPRYISCC -TFIQTASTQTYAANVVVH-PLPQVUSPC 219

Query 236 AYARIAJKLQCGAPGPGRERAAAPRASRRRARRVVMIVNUVVALE- -PTLSWMLPMLWALLII 293
Y RI+ + OR A + W + P + W + L + L +
Sbjct 220 YETATWLVULJJKRKA-----KPSERLCKLPSDLRSPFLNPVVF+PFAPIKMLPQIGLCAV 274

Query 294 DVGFLWVWVWVLTWVYPAFFWVHAFPNNSAM+IYGVHMPERPGOAFARFLCPR- 351
Sbjct 275 AINQPMQMAP- -IPEGFLGVYVSIYLAYPNSCLNAIVYGLA+QNPFREYKRILLALMNPNRH 331

Query 352 -----PSRSKWE 359
Sbjct 332 CIQDASKGKSHAG 344

```

```
>ref[NP_001043.2] |UG| somatostatin receptor 4 [Homo sapiens]
sp|P11391.2|[SSKR_HUMAN] |G| RecName: Full-Somatostatin receptor type 4; AltName: Full-SS4R
|CAB51953.1| |G| somatostatin receptor 4 [Homo sapiens]
gb|AAII17271.1| |G| Somatostatin receptor 4 [Homo sapiens]
```

(Over 10 PubMed links)

Score = 113 bits (283), Expect = 1e-24, Method: Compositional matrix adjust.  
Identities = 92/306 (30%), Positives = 150/306 (49%), Gaps = 34/306 (11%)

Query 50 YALIFLICMVGNTLVCFLVILNRHMHTVNMFLINLAWSDLVLGICFMPTTLVDNLITL0H 109  
YAL + Lt + VGR LV F++ L M T TN+++LNLAV=L L + \*P + N  
Sbjct 54 YALCVLVGLGNALQVNVLQVFLVYLRYKAMRKTATNLYLNLAVALADELF -MLSVPFVASSAALRHW 112

Query 110 PFDNATCNSGMSVQMSVSASVPTLVAIAVIERFRCIVHPFPREKLTLRKALVLTIAV--IMA 167  
PF + C + V G+++ SVF L ++V+R+ +VHP R R ++ + \*W  
Sbjct 113 PGFSVLCRALVLSVGDLNAMPFLCFLVLSVDYRVAVVHPLRAATYRRPSVAKLNLINLGWL 172

Query 168 LALLINCPSPASVTLTVTREEHHFMDAR--NRSYPLYSCEWAPKEKGMRVRVTTLFISHYL 226  
+L+ P A+ D R R -C W P V+ F +L  
Sbjct 173 ASLVLTVLPIAI-----FADTRPARGGQAVACNLQWHPPAMSAVFPVVTFLLGFL 221

Query 227 APALALIVVMARYARIKLCQAGPAGGEEAADPDRASRERA--RVVHMLVMVALFTLMSW 284  
P+ I + Y I K+ A G++ RR++ ++ ++MV + F L W+  
Sbjct 222 LPVLAIGLCLYLGVKN-RVALRALRAGWQQ-----RRRSEKKITRLVLAHVVFVLCNM 273

Query 285 PLMALLL-IDYQOLSAPOHLVTVAPPFAWMFLAFPNSSANAPIYGVFHNFRRGFOAA 343  
P + LL + L A H+ + L+ NS AMPI:YG+ +NFRR FQ  
Sbjct 274 PFYVVCQJLNLFPVTSLDATVNHWSLI-----LSTYANSANCPILYGFISDNFRFFFQRV 325

Query 344 PRARIC 349  
Sbjct 326 LCLRC 331

>gb|AAN87342.1| [C] DRG kappa 1 splice variant KOR 1A [Homo sapiens]  
Length=366

Gene ID: 4986 OPRE1 | opioid receptor, kappa 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 113 bits (283), Expect = 1e-24, Method: Compositional matrix adjust.  
Identities = 97/340 (28%), Positives = 164/340 (48%), Gaps = 40/340 (11%)

Query 8 PPNSWPQLSQNGQTNTTATATLNTFESYYQUNPSPVAMPMIVA-YALIFLICMVGNTLVC 66  
PPNS-----HSP-----P-----V-----P-----V-----P-----V-----P-----F 68  
Sbjct 23 -----AGSEDALQHPA-----HISPAIPWIIITAVYVSVVPGVLGVHSNLVNF 68

Query 67 IVLKHRRHMFVTVLNLALAVELDINGIFCMPTTLVDNLITLHGPFTPS-TCKMSGLVQGMGS 126  
+L+ M T TN++I L NL+D L+ MP + L+ W+P + S+ CKW + P 127  
Sbjct 69 VIIRYTKEMKATATHIYIPFLNLADLTVLT-TMPFQSTVLYLMMNSWPFDALCKIVISIDYNN 127

Query 127 VSAASVFLVIAVIERFRCIVHPFPREKLTLR---KALVIAVINAALALIMCPASVLTATV 183  
+S+PTL +V+R+ +V+R+ +P+ +S+ +S+ +L+ +S+ +S+ +L+ +T 183  
Sbjct 128 MFTSIPFLTMWSVSDYRIAVCHPVK-ALDFRPTPLKAKIINICIMLLESSLSSVQI-SVBLVQGT 185

Query 184 REEHHHFMUDARNRSGP---LWSQWENPPEKGMRVRYTTTFSHIVYIAPLALIUVVWVARIA 241  
Sbjct 186 KVEDRDWDVIEC+E+P+Y MS++ +V+P+ +V+P+ +V+P+ +V+P+ +V+Y+ 237

Query 242 KLGQAPGAPGEEAADPDRASRERAIVPFLVJALJPTLQWLPWMAILLLIDYQOLSP 301  
+L+ +G E R R+ +V+V F +W P+ +L+ G S  
Sbjct 238 RL-KSVVELLGGSGRE-----KSDNLRLPITRILVLLVVAFFVCFWTFIHIPILVBEALGSTSHS 291

Query 302 QIHWLTVY+PFAWMFLAFPNSSANAPIYGVFHNFRRGFO 341  
Sbjct 292 TAALLSYY---FCIALGYTNSSLMPILYAFLEMFRFCR 328

>gb|EAX10169.1| [C] somatostatin receptor 4, isoform CRA\_b [Homo sapiens]  
Length=398

Gene ID: 6754 SSTR4 | somatostatin receptor 4 [Homo sapiens]  
(Over 10 PubMed links)

Score = 113 bits (283), Expect = 1e-24, Method: Compositional matrix adjust.  
Identities = 92/306 (30%), Positives = 150/306 (49%), Gaps = 34/306 (11%)

Query 50 YALIFLICMVGNTLVCFLVILNRHMHTVNMFLINLAWSDLVLGICFMPTTLVDNLITL0H 109  
YAL + Lt + VGR LV F++ L M T TN+++LNLAV=L L + \*P + N  
Sbjct 54 YALCVLVGLGNALQVNVLQVFLVYLRYKAMRKTATNLYLNLAVALADELF -MLSVPFVASSAALRHW 112

Query 110 PFDNATCNSGMSVQMSVSASVPTLVAIAVIERFRCIVHPFPREKLTLRKALVLTIAV--IMA 167  
PF + C + V G+++ SVF L ++V+R+ +VHP R R ++ + \*W  
Sbjct 113 PGFSVLCRALVLSVGDLNAMPFLCFLVLSVDYRVAVVHPLRAATYRRPSVAKLNLINLGWL 172

Query 168 LALLINCPSPASVTLTVTREEHHFMDAR--NRSYPLYSCEWAPKEKGMRVRVTTLFISHYL 226  
+L+ P A+ D R R -C W P V+ F +L  
Sbjct 173 ASLVLTVLPIAI-----FADTRPARGGQAVACNLQWHPPAMSAVFPVVTFLLGFL 221

Query 227 APALALIVVMARYARIKLCQAGPAGGEEAADPDRASRERA--RVVHMLVMVALFTLMSW 284  
P+ I + Y I K+ A G++ RR++ ++ ++MV + F L W+  
Sbjct 222 LPVLAIGLCLYLGVKN-RVALRALRAGWQQ-----RRRSEKKITRLVLAHVVFVLCNM 273

Query 285 PLMALLL-IDYQOLSAPOHLVTVAPPFAWMFLAFPNSSANAPIYGVFHNFRRGFOAA 343  
P + LL + L A H+ + L+ NS AMPI:YG+ +NFRR FQ  
Sbjct 274 PFYVVCQJLNLFPVTSLDATVNHWSLI-----LSTYANSANCPILYGFISDNFRFFFQRV 325

Query 344 PRARIC 349  
Sbjct 326 LCLRC 331

>emb|CANH3066.1| [C] prolactin releasing hormone receptor [Homo sapiens]  
Length=370

Gene ID: 2834 PRHLH | prolactin releasing hormone receptor [Homo sapiens]  
(Over 10 PubMed links)

Score = 113 bits (283), Expect = 1e-24, Method: Compositional matrix adjust.  
Identities = 99/305 (32%), Positives = 152/305 (49%), Gaps = 25/305 (8%)

Query 60 GHTLVCFIVLNRHMHTVNMFLINLAWSDLVLGICFMPTTLVDNLITL-TGWPFDNATCK 118

Sbjct	77	GN L- + + R + VTN I NLA+SD+L- C+P TL	GN P	C +	136
		GNCLLVLVIAVRERLNLNPTFLNGLQNLSDLVLMCTACVPLTLAYAPEGVFFGGGLCHL			
Query	119	SLGVLGVGSVSAVSFTLVAJERFPCVLRPFKRLTLLRALKVLTAVWALLNNIMCPSSA			178
		-O+ +V SVTF TAV+R+ +VIR R + +LR + + +IHAL + +P+AV			
Sbjct	137	VFFLPDTPTVYVSVFTLTLTIDRVYVWPLURRSLRSASVATLNAWSALPANV			196
Query	179	TLTLYTREESHHWPM/DARNYLSPYLSCRMAR-PEKGKMRVTTVFLSHYILPLALATVYMYA			237
		H + V+ C + K E C W + R + Y + L YL D + I+++			
Sbjct	197	- - - - -HTHVLKPLWPHVUL- - - - -CEFGNSQGRRQGUTMAGLNGVLLVTPPLVLLSIV			246
Query	238	RIARKLQCGQPGAPGCGAEADPASPRRSHRVRVMMUWLPAVFLPSLWMLAWALNDLIDQY			297
		R++ KI P + AD + RER + LV++ + F + MLP + L + D			
Sbjct	247	RSVSKLNRNNVPPGCVTOSQADMRARRRKRRRTRFC-LUVV+VUVFVACMLPLVFNRLRDLDP			305
Query	298	LSAPQHLLTVTYVFP---FAHWLAFNNPSANPIYIGYNPNFPRCPQQAFAFRALCRPRS			353
		H + Y HLLA ++ NN + I+ +PR + A + CPR			
Sbjct	306	--HAIDPYIAFGQLVQLCHWLAMSSACYNPFYIAMLHDSFREELRLLVAV--PRKI			357
Query	354	GSKHE 356			
		H +			
Sbjct	358	APIGQ 362			

>dbj|BAF82684.1| G unnamed protein product [Homo sapiens]  
Length:384

Page 204

zab|AAA60565.1| G somatostatin receptor

Length=388

>dbj|BAG60542.1| G unnamed protein product (Homo sapiens)

Length=184

Query 134 LVAIAVERFRCIVHPFREKLRLRALKALVIAVALALLNCPSAVTLTVTRE-EHHFMDV 192  
 LV IAVER + I+P+ + R A V IAVL LA+ P + + T E + + D LV  
 Sbjct 61 LVLIAVERHQLIINPRGWNPNNRHAYIGIAVIAVLAVALSLPFLYQVNTPEFPQNVL 120

Query 193 ARNRSYPLSYCEAMPKGMRVYTFVLFSHYIPLALIVVMYARIAKRL 243  
 A Y C++ +P R YTT+L Y PL I + Y ++ EKL  
 Sbjct 121 AYKDK--YVCFDQFSPDSHRLSYYTLLLVLQYFGPLCPICYKV-RKL 167

>gb|AAU21070.1|AF498922\_1 | G opioid receptor kappa [Homo sapiens]  
 gb|AAA20985.1| G kappa opioid receptor  
 dbj|BAG35888.1| G unnamed protein product [Homo sapiens]  
 Length=380

Gene ID: 4986 OPRK1 | opioid receptor, kappa 1 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 110 bits (276), Expect = 6e-24, Method: Compositional matrix adjust.  
 Identities = 89/310 (28%), Aligned = 54/310 (49%), Gaps = 26/310 (8%)

Query 38 HTSPVAAAMPITVA-IALYPLILMVNGNTLWCP1VLKQRHMHTTNMFIILNLAVSDLLVGIFC 96  
 H SP + + I A Y++F++ +VGN+LV F++++ M T TH+I NLA+D LV  
 Sbjct 53 HISPAIPWIIATVAVSVVVFGVLGVNGLSNMWFVIIYRTMKTATNHYIPNLALADALVT-T 111

Query 97 MPTLTVDNLITGHPPDNATCKMSGLVQGMGSVASVFTLVAIAVERFRCIVHPFREKLRL 156  
 MP L WPF + CK+ + ++ S+TFL ++V+R+ + HP + L R  
 Sbjct 112 MPFQSTVYLMNSMPKGDVKLCIVISIDYNNMFTSISFLTMWSVODVYIAVCHPVK- ALDFR 170

Query 157 ---KALVITIAVIAVALALLNCPSAVTLTVTREHHFPMVDARNNSYP---LYSCHEANPKEG 211  
 KA + + IM L+ + SA+ L+ V + + P + PS YS W+ +  
 Sbjct 171 TPLKAKINICIMLSSVSGI-SAIVLGGTQVREDDVIECSIQFPDDDSYNSWDLFPMK- 227

Query 212 MRRVYTTLVFLPSIYLAPLALIYVMMYARIAKRLQOQPGPAPGGEADPRASRRARVHIM 271  
 +P + ++ P+ +I+V Y + + L++ + G E R R+ +  
 Sbjct 228 ---ICVPFIAFPVIPV1WVCYTIMLIRL-KSVRLLSGSRE-----KDRNLRLRITRL 275

Query 272 LIVVVALPFTLSMLPLWALLLIDYQGQISAPQLHVLTIVYAFFFAHWLAFPFNSANIIYGY 331  
 +++V + P + W P+ +I+ G S S L + Y F L + NSS NPI+Y +  
 Sbjct 276 VLVVAVVFVCWNTPIHIFILVREALGSTSHSTAALSSYY---FCIALGYTNSSLNPILYAF 332

Query 332 FNENFRRGFQ 341  
 \*ENF-R F+  
 Sbjct 333 LDENFKRCFR 342

>ref|NP\_000903.2| G opioid receptor, kappa 1 [Homo sapiens]  
 sp|P41145.2|OPRX\_HUMAN | G RecName: Full=Kappa-type opioid receptor; AltName: Full=KOR-1  
 gb|AAC50158.1| G kappa opioid receptor  
 gb|AAE63906.1| G kappa opioid receptor  
 gb|AAH99912.1| G Opioid receptor, kappa 1 [Homo sapiens]  
 gb|BAW86723.1| G opioid receptor, kappa 1 [Homo sapiens]  
 prf|2104381A kappa opioid receptor  
 Length=380

Gene ID: 4986 OPRK1 | opioid receptor, kappa 1 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 110 bits (276), Expect = 7e-24, Method: Compositional matrix adjust.  
 Identities = 89/310 (28%), Aligned = 54/310 (49%), Gaps = 26/310 (8%)

Query 38 HTSPVAAAMPITVA-IALYPLILMVNGNTLWCP1VLKQRHMHTTNMFIILNLAVSDLLVGIFC 96  
 H SP + + I A Y++F++ +VGN+LV F++++ M T TH+I NLA+D LV  
 Sbjct 53 HISPAIPWIIATVAVSVVVFGVLGVNGLSNMWFVIIYRTMKTATNHYIPNLALADALVT-T 111

Query 97 MPTLTVDNLITGHPPDNATCKMSGLVQGMGSVASVFTLVAIAVERFRCIVHPFREKLRL 156  
 MP L WPF + CK+ + ++ S+TFL ++V+R+ + HP + L R  
 Sbjct 112 MPFQSTVYLMNSMPKGDVKLCIVISIDYNNMFTSISFLTMWSVODVYIAVCHPVK- ALDFR 170

Query 157 ---KALVITIAVIAVALALLNCPSAVTLTVTREHHFPMVDARNNSYP---LYSCHEANPKEG 211  
 KA + + IM L+ + SA+ L+ V + + P + PS YS W+ +  
 Sbjct 171 TPLKAKINICIMLSSVSGI-SAIVLGGTQVREDDVIECSIQFPDDDSYNSWDLFPMK- 227

Query 212 MRRVYTTLVFLPSIYLAPLALIYVMMYARIAKRLQOQPGPAPGGEADPRASRRARVHIM 271  
 +P + ++ P+ +I+V Y + + L++ + G E R R+ +  
 Sbjct 228 ---ICVPFIAFPVIPV1WVCYTIMLIRL-KSVRLLSGSRE-----KDRNLRLRITRL 275

Query 272 LIVVVALPFTLSMLPLWALLLIDYQGQISAPQLHVLTIVYAFFFAHWLAFPFNSANIIYGY 331  
 +++V + P + W P+ +I+ G S S L + Y F L + NSS NPI+Y +  
 Sbjct 276 VLVVAVVFVCWNTPIHIFILVREALGSTSHSTAALSSYY---FCIALGYTNSSLNPILYAF 332

Query 332 FNENFRRGFQ 341  
 \*ENF-R F+  
 Sbjct 333 LDENFKRCFR 342

>gb|AAN32829.1|AF441129\_1 | G cholecystokinin-C receptor [Homo sapiens]  
 gb|AAK38351.1| G CCK-B/gastrin receptor variant [Homo sapiens]  
 Length=516

Gene ID: 887 CCKBR | cholecystokinin B receptor [Homo sapiens]  
 (Over 10 PubMed links)

Score = 110 bits (276), Expect = 8e-24, Method: Compositional matrix adjust.  
 Identities = 69/202 (34%), Aligned = 107/202 (52%), Gaps = 13/202 (6%)

Query 44 ANFIVAYALIPLCMNGNTLWCP1VLKQRHMHTTNMFIILNLAVSDLLVGIFGOMPTTLLVD 103  
 A+ I YA+IPL+ + GN L+ ++ + R + TTV+ P+L+LA+VSDLL+ + CMP TL+  
 Sbjct 55 AIRITLYAVIPLMSVGGMNLIIWVLRSLRRTVNAFLSLA+VSDLLAVACMPFTLLP 114

Query 104 NLITGWPFDNATCKMSGLVGVMSVASQVFTLVAIAVERFRCIVHPFREKL-TLRLKALVT 161  
 NL+ + F CK + G+S VS S +LVAIA+ER+ I P + ++ T A

Sbjct 115 NLNGTFPIGTICKAVASYLNGVSVSVSTLSLVAIALERYSAICRPIQARVWQTRSAAKV 174  
 Query 162 IAVIMVALALILMCPSPAVTIVTREHHHFWDVARNSYSPLYSCWEAMPEKGMGRVVTTVLF 221  
 C W R + R + + L  
 Sbjct 175 IATWMLL@GLLMWPPVYTTVQPGPVRV-----QCVHRRMPASRARQTMWSVLL 223  
 Query 222 SHYLAPEALVVMVYARIAKL 243  
 Sbjct 224 LLJFFIPGV@AVAYGLISREL 245

Score = 43.9 bits (102), Expect = 0.001, Method: Compositional matrix adjust.  
 Identities = 26/94 (27%), Positives = 46/94 (48%), Gaps = 6/94 (6%).  
 Query 246 APGPAPOGEGEADPRASRRARVWVHMLWVMPALVFTPLSMLPWALLLIDYQQLSAPOLH 305  
 APCP G + + + R VV ML+ + + F L MLP+ + + P H  
 Sbjct 380 APGPGSGSKPTQAKMLAKKR -VVRMMLWIVLFLFLMLPVYS---ANTWRAPDQGPAHR 434  
 Query 306 VTVYA-FPPPARMLAFNNSANPILYGYFENFER 338  
 Sbjct 435 ALSGPAPISPIHLLSYASACVNPLVYCFPMHRRFRQ 468

>gb|BAM68734.1| **G** cholecystokinin B receptor, isoform CRA\_a [Homo sapiens]  
Length=516

GENE ID: 887 **CCKBR** | cholecystokinin B receptor [Homo sapiens]  
(Over 10 PubMed links)

Score = 110 bits (275), Expect = 1e-23, Method: Compositional matrix adjust.  
Identities = 69/202 (34%), Positives = 107/202 (52%), Gaps = 13/202 (6%).

Query 44 ANPITAYALIPLLQFVLLQVTPCIVLIVNHWVITVNPFLNLAVSDELJVGICPOMPTLWD 103  
 APCP G + + + R VV ML+ + + F L MLP+ + + P H  
 Sbjct 55 IATWMLL@AVIPM+GN L+ + + R + TVIN F1:L@LVSDDL@ + CMP T@L 114  
 Query 104 NLITGWFDPNATCQMSGVLQVGSVASVFTLVAIAVERPCTIWPFREKL -TLRKALVT 161  
 APCP G + + + R VV ML+ + + F L MLP+ + + P H  
 Sbjct 115 NLNGTFPIGTICKAVASYLNGVSVSVSTLSLVAIALERYSAICRPIQARVWQTRSAAKV 174  
 Query 162 IAVIMVALALILMCPSPAVTIVTREHHHFWDVARNSYSPLYSCWEAMPEKGMGRVVTTVLF 221  
 C W R + + + L  
 Sbjct 175 IATWMLL@GLLMWPPVYTTVQPGPVRV-----QCVHRRMPASRARQTMWSVLL 223  
 Query 222 SHYLAPEALVVMVYARIAKL 243  
 Sbjct 224 LLJFFIPGV@AVAYGLISREL 245

Score = 43.9 bits (102), Expect = 0.001, Method: Compositional matrix adjust.  
Identities = 26/94 (27%), Positives = 46/94 (48%), Gaps = 6/94 (6%).

Query 246 APGPAPOGEGEADPRASRRARVWVHMLWVMPALVFTPLSMLPWALLLIDYQQLSAPOLH 305  
 APCP G + + + R VV ML+ + + F L MLP+ + + P H  
 Sbjct 380 APGPGSGSKPTQAKMLAKKR -VVRMMLWIVLFLFLMLPVYS---ANTWRAPDQGPAHR 434  
 Query 306 VTVYA-FPPPARMLAFNNSANPILYGYFENFER 338  
 Sbjct 435 ALSGPAPISPIHLLSYASACVNPLVYCFPMHRRFRQ 468

>gb|BAX05261.1| **G** G protein-coupled receptor 103, isoform CRA\_a [Homo sapiens]  
Length=258

GENE ID: 84109 QRPPR | pyroglutamylated RFamide peptide receptor [Homo sapiens]  
(10 or fewer Published links)

Score = 110 bits (274), Expect = 1e-23, Method: Compositional matrix adjust.  
Identities = 62/181 (34%), Positives = 101/181 (55%), Gaps = 8/181 (4%).

Query 51 ALIFLFLCGNTLWCIVLWVNHMHHTVNTMPLIILNAVSDELJVGICPOMPTLWDNLITGWP 110  
 APCP G + + + R VV ML+ + + F L MLP+ + + P H  
 Sbjct 53 VVPLALPFGNALPVVPTVRSKAMRTVTNIPICSLALSDLILITPPCIPVMTQUNISDNWL 112  
 Query 111 FONATCKM95GLVQGMESVASSPFTLVAIAVERPCTIWPFREKL -TLRKALVTIAVIAL 168  
 APCP G + + + R VV ML+ + + F L MLP+ + + P H  
 Sbjct 113 QGAFCIKCMVMPPEVQ-VVPLALPFGNALPVVPTVRSKAMRTVTNIPICSLALSDLILITPPCIPVMTQUNISDNWL 172  
 Query 169 AJJIMCPASVTLTIVTREHHHFWDVARNSYSPLYSCWEAMPEKUMMRVTVTFPSHISYIAP 228  
 APCP G + + + R VV ML+ + + F L MLP+ + + P H  
 Sbjct 173 AVIVGSPHMWVHQQLKXIDYQDLYPSKEH----ICCLEBWTSPVHQKIIYTTTFLVILPFLP 226  
 Query 229 L 229  
 Sbjct 227 L 227

>ref|NP\_795344.1| **G** cholecystokinin B receptor [Homo sapiens]  
 sp|P32239.1|GASR\_HUMAN **G** RecName: Full=Gastrin/cholecystokinin type B receptor; Short=CCK-B receptor; Short=CCK-8 receptor; Short=CCK2-R  
 gb|AAA35660.1| **G** cholecystokinin receptor  
 10 more sequence titles

gb|AAA35657.1| **G** cholecystokinin-B/gastrin receptor  
 gb|AAC7528.1| **G** gastrin receptor  
 dbj|BA002564.1| **G** cholecystokinin receptor [Homo sapiens]  
 gb|AAH00740.1| **G** Cholecystokinin B receptor [Homo sapiens]  
 dbj|AAH04759.2| **G** cholecystokinin-B receptor/gastrin receptor [Homo sapiens]  
 gb|AAP35435.1| **G** cholecystokinin B receptor [Homo sapiens]  
 gb|AAP84364.1| **G** cholecystokinin B receptor [Homo sapiens]  
 Length=447

GENE ID: 887 CCKBR | cholecystokinin B receptor [Homo sapiens]  
 (Over 10 PubMed links)

Score = 110 bits (274), Expect = 1e-23, Method: Compositional matrix adjust.  
 Identities = 69/202 (34%), Positives = 170/202 (52%), Gaps = 13/202 (6%)

Query 44 AMTIVAYALIPLLCMVGNTLVCPIVLCNPNFLAVSDLLWLGICPOMPFTLVD 103  
 Sbjct 55 A+ I\_ Y+A+PL+ +G+V+ ++\_R+ TTVN F+L+LA+VS+D+L+ + CMP TL+ 103  
 Sbjct 55 AIRITLYAVIPLMSVGGNNLMLVVLGLSLRRTVNTLSSLSLAVASLLAVALCPTFLPP 114

Query 104 NLITGMPFDNATCAGSGLVQOMSVSVAASVPTLVAVIAVERFRCIVHPPEKEL- -TLRKALVT 161  
 Sbjct 115 NL+GTPFIVOTVICKASVYLSVGSVSVS+VSTLSLVAIALERYSAICRPLQARVMQTRSHAARV 174

Query 162 IAVIVAYALALLIMCPASPAVLTIVTREEEHHPMVDAARNESYPLYSCEAMPEKGMRRVVTTVLF 221  
 Sbjct 175 IAVTMLLSLCLMVPYPPVYTTVQPVGPVRV-----QCVRHRWPSARVRQTWSVLL 223

Query 222 SHYIYLAPLALIVVMMYARIKL 243  
 Sbjct 224 LLLFFIPGVNVMAVAYGLISREL 245

Score = 44.3 bits (103), Expect = 7e-04, Method: Compositional matrix adjust.  
 Identities = 26/94 (27%), Positives = 46/94 (48%), Gaps = 6/94 (6%)

Query 246 APGPAPGGEAEADPRASRRARVRYHMDWVWVVALFPFLSHLWLPWALLLLLIDYQQLSAPOPQLHL 305  
 Sbjct 311 APGPOSGSRPTQAKLLAKR-----VWVHMLLIVVLFCLWLPVYS---ANTMRADPGPGGAHR 365

Query 306 VTVYA-FPPAHMLAFLPFNSSANPIIYGYNENFPR 338  
 Sbjct 366 ALSGAPISPFHILSYASACVNPMVYCPWHRFRP 399

>gb|AAAB30766.2| C cholecystokinin B receptor [Homo sapiens]  
 Length=447

GENE ID: 887 CCKBR | cholecystokinin B receptor [Homo sapiens]  
 (Over 10 PubMed links)

Score = 109 bits (273), Expect = 1e-23, Method: Compositional matrix adjust.  
 Identities = 69/202 (34%), Positives = 107/202 (52%), Gaps = 13/202 (6%)

Query 44 AMTIVAYALIPLLCMVGNTLVCPIVLCNPNFLAVSDLLWLGICPOMPFTLVD 103  
 Sbjct 55 A+ I\_ Y+A+PL+ +G+V+ ++\_R+ TTVN F+L+LA+VS+D+L+ + CMP TL+ 103  
 Sbjct 55 AIRITLYAVIPLMSVGGNNLMLVVLGLSLRRTVNTLSSLSLAVASLLAVALCPTFLPP 114

Query 104 NLITGMPFDNATCAGSGLVQOMSVSVAASVPTLVAVIAVERFRCIVHPPEKEL- -TLRKALVT 161  
 Sbjct 115 NL+GTPFIVOTVICKASVYLSVGSVSVS+VSTLSLVAIALERYSAICRPLQARVMQTRSHAARV 174

Query 162 IAVIVAYALALLIMCPASPAVLTIVTREEEHHPMVDAARNESYPLYSCEAMPEKGMRRVVTTVLF 221  
 Sbjct 175 IAVTMLLSLCLMVPYPPVYTTVQPVGPVRV-----QCVRHRWPSARVRQTWSVLL 223

Query 222 SHYIYLAPLALIVVMMYARIKL 243  
 Sbjct 224 LLLFFIPGVNVMAVAYGLISREL 245

Score = 44.7 bits (104), Expect = 7e-04, Method: Compositional matrix adjust.  
 Identities = 26/94 (27%), Positives = 46/94 (48%), Gaps = 6/94 (6%)

Query 246 APGPAPGGEAEADPRASRRARVRYHMDWVWVVALFPFLSHLWLPWALLLLLIDYQQLSAPOPQLHL 305  
 Sbjct 311 APGPOSGSRPTQAKLLAKR-----VWVHMLLIVVLFCLWLPVYS---ANTMRADPGPGGAHR 365

Query 306 VTVYA-FPPAHMLAFLPFNSSANPIIYGYNENFPR 338  
 Sbjct 366 ALSGAPISPFHILSYASACVNPMVYCPWHRFRP 399

>ref|NP\_001040.1| C somatostatin receptor 1 [Homo sapiens]

sp|P30872.1|SSRI HUMAN C RecName: Full-Somatostatin receptor type 1; AltName: Full-SS1;  
 AltName: Full-SST1-2  
 9 more sequences in this file

gb|AAA58247.1| C somatostatin receptor isoform 1

gb|AAH35618.1| C Somatostatin receptor 3 [Homo sapiens]

gb|AAP84349.1| C somatostatin receptor 1 [Homo sapiens]

gb|EAW65836.1| C somatostatin receptor 1 [Homo sapiens]

Length=391

GENE ID: 6751 SSTR1 | somatostatin receptor 1 [Homo sapiens]

(Over 10 PubMed links)

Score = 109 bits (273), Expect = 1e-23, Method: Compositional matrix adjust.  
 Identities = 87/330 (26%), Positives = 160/330 (48%), Gaps = 44/330 (13%)

Query 16 SGQNTTEATPATNLTFPSSYYQHTSPVAMPVAYALIPLLCMVGNTLVCPIVLCNPNFLAVSDLLWLGICPOMPFTLVD 75  
 Sbjct 46 SGQNT+E S + FT Y+++ L+ +GN+V+++L+ M 90  
 Sbjct 55 SGQNTLSBEG-----QGSVAILISIPI-YSVCLVGLCONSMVIVYLYRAKMK 90

Query 76 TVTNMPFLAVSDLLWLGICPOMPFTLVDNLITGMPFDNATCAGSGLVQOMSVSVAASVPTLV 135  
 Sbjct 91 T+TN+I+LNL+A+L+ +MPF C++ V ++ S+ L 135  
 Sbjct 91 TATINYIYLGAATD-MLSVPFLVITSLRHPFLGALLCRVLVLSVDA+TTSYICLT 149

Query 136 AIAVERFRCIVHPPEKELTLRALKALVTI--IWAALALLIMCPASPAVLTIVTREEEHHPMVDA 193  
 Sbjct 150 VLSCDRTYVAVHPIKAARYRPVTKAVKVNVLGVWVLSLIVLPIVY-----PSRTA 199

Query 194 RRNSYPLYSNCWAEPEKGMRRVYTTVHSHI--YIAPLALIVVMMYARIKLOAAGPAP 251  
 Sbjct 224 N S + C PE V++ L+ P+ I+ Y+ K+ 251

Sbjct 200 AN-SDGTVACNMLMPPEPAQRWLVGFVLYTFLNGPLLPGAICLCYVLLIAKMRM----- 253  
 Query 252 GGEAEADPRASRRRARRVHMLVMVALPFTLSHLPLWALLLIDYQQLSAPOLHLVTVYAF 311  
 Sbjct 254 -ALQJGWWQQRKRSERKITLWVWVWVFPVICWMPFYYVGLVNVPABQDDATVSQSLSVI-- 310  
 Query 312 PFAHWLAFPNNSANPIIYGYPNDFNRFGQ 341  
 Sbjct 311 ----LOVANSCANPILYFLSDUNPKRSPQ 335

>gb|EAW68735.1| C cholecystokinin B receptor, isoform CRA\_b [Homo sapiens]  
 Length=447  
 GRNE ID: 887 CCKBR | cholecystokinin B receptor [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 109 bits (273), Expect = 2e-23, Method: Compositional matrix adjust.  
 Identities = 69/202 (34%), Positives = 107/202 (52%), Gaps = 11/202 (6%)  
 Query 44 ANFTAVALIFLLCNVENTLWCFITVLWNRRHMMTTVTNNFTFLNLAVSDLNLVGHFCMPPTLVD 103  
 Sbjct 55 AIRITLVAVIFLMSVGGNMNLITVIGLSRRLTVTNAFILSLSLAVSDLLLAVACMPFTLIP 114  
 Query 104 NLITGWPFDNATCNSGGLVQOMSVSASVFTIWAIAINERFRCIVHPFREKL---PLRKALVLT 161  
 Sbjct 115 NMAGTFIPOTIICKAVSVLIMVSVSVSVSTLISLVAIALERYSACIRPLQARVNQTRSHAARV 174  
 Query 162 IAVTMALALLIMCPSPAVTPTVTREEHHPMV/DARNNSYPLYSCEAHPERKMBRVVTTVLP 221  
 Sbjct 175 IVATMILSCLLMVPPVYTYVQPGVCPVLT-----QCVRHRWPSARVRQTMSVLLL 223  
 Query 222 SHIYLAPLALIIVMVYARIAREKL 243  
 Sbjct 224 LLLFFIPGVVMAVAYGLISREL 245

Select All Get selected sequences Distance tree of results